

SEQUENCE LISTING

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Erker, James C
Desai, Suresh M
Dawson, George J
Mushawar, Isa K

<120> METHODS AND COMPOSITIONS FOR DETECTING HEPATITIS E
VIRUS

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<150> US 09/173,141

<151> 1998-10-15

<160> 258

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Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
85 90 95	
tgt ttc ctt aga ccg gtt ggc cga gat gtt cag cgc tgg tac tct gcc	336
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggc cct gcg gct aat tgc cgc cgc tcc gcg ttg cgt ggt	384
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc ccc ccc gct gac cgc act tac tgc ttt gat gga ttc tcc cgt tgt	432
Leu Pro Pro Ala Asp Arg Thr Tyr Cys Phe Asp Gly Phe Ser Arg Cys	
130 135 140	
gct ttt gct gca gag acc ggt gtg gct ctt tac tct ctg cat gac ctt	480
Ala Phe Ala Ala Glu Thr Gly Val Ala Leu Tyr Ser Leu His Asp Leu	
145 150 155 160	
tgg cca gct gat gtt gca gag gct atg gcc cgc cac ggg atr aca cgc	528
Trp Pro Ala Asp Val Ala Glu Ala Met Ala Arg His Gly Xaa Thr Arg	
165 170 175	
ttg tat gcc gca ctg cac ctt ccc cct gag gtg ctg cta cca ccc ggc	576
Leu Tyr Ala Ala Leu His Leu Pro Pro Glu Val Leu Leu Pro Pro Gly	
180 185 190	
acc tac cac aca acc tcg tat ctc ctg att cac gac ggc gac cgc gct	624
Thr Tyr His Thr Thr Ser Tyr Leu Leu Ile His Asp Gly Asp Arg Ala	
195 200 205	
gtt gta act tac gag ggc gat act agt gcg ggc tat aat cat gat gtc	672
Val Val Thr Tyr Glu Gly Asp Thr Ser Ala Gly Tyr Asn His Asp Val	
210 215 220	
tcc ata ctt cgt gcg tgg atc cgt act aca aaa ata gtt ggt gat cat	720

Ser	Ile	Leu	Arg	Ala	Trp	Ile	Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His	
225					230					235					240	
ccg	ttg	gtc	ata	gag	cgt	gtg	cgg	gcc	att	gga	tgt	cat	ttt	gtg	ttg	768
Pro	Leu	Val	Ile	Glu	Arg	Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	
				245				250						255		
ctg	ctc	acc	gca	gcc	cct	gag	ccg	tca	ccc	atg	cct	tat	gtt	cct	tac	816
Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	
			260					265					270			
cct	cgt	tca	acg	gag	gtg	tat	gtc	cgg	tcc	ata	ttt	ggc	cct	ggc	ggc	864
Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	
			275				280					285				
tcc	cca	tcc	ttg	ttt	ccg	tca	gcc	tgc	tct	act	aaa	tct	act	ttc	cat	912
Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	
			290			295					300					
gct	gtc	ccg	gtg	cat	atc	tgg	gat	cgg	ctc	atg	ctc	ttt	ggg	gcc	acc	960
Ala	Val	Pro	Val	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr	
305					310					315					320	
ctg	gac	gat	cag	gcg	ttt	tgc	tgt	tca	cgg	ctc	atg	act	tac	ctc	cgt	1008
Leu	Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	
				325					330					335		
ggg	att	agt	tac	aag	gtc	act	gtc	ggc	gcg	ctt	gtc	gct	aat	gag	ggg	1056
Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly	
			340					345					350			
tgg	aac	gcc	tct	gaa	gac	gct	ctt	act	gca	rtg	atc	act	gca	gct	tat	1104
Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Xaa	Ile	Thr	Ala	Ala	Tyr	
			355				360					365				
ttg	act	att	tgc	cat	cag	cgt	tat	ctc	cgc	acc	cag	gcg	ata	tcc	aag	1152
Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	
			370			375					380					
ggc	atg	cgc	cgg	ttg	ggg	ggt	gag	cac	gcc	cag	aaa	ttt	atc	aca	aga	1200
Gly	Met	Arg	Arg	Leu	Gly	Val	Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	
385					390					395					400	
ctc	tac	agt	tgg	cta	ttt	gag	aag	tct	ggc	cgt	gat	tat	atc	ccc	ggc	1248
Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	
				405					410					415		
cgc	cag	ctt	cag	ttc	tat	gca	cag	tgc	cga	cgg	tgg	cta	tct	gca	ggc	1296
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	
			420					425					430			
ttc	cac	cta	gac	ccc	agg	gta	ctt	ggt	ttt	gat	gag	tca	gta	cca	tgc	1344
Phe	His	Leu	Asp	Pro	Arg	Val	Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys	
			435				440					445				
cgc	tgt	agg	acg	ttt	ttg	aag	aaa	ggt	gcg	ggg	aaa	ttc	tgc	tgt	ttt	1392
Arg	Cys	Arg	Thr	Phe	Leu	Lys	Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe	

450	455	460	
atg cgg tgg ctc ggg cag gag tgt acc tgc ttc ttg gag ccg gcc gag Met Arg Trp Leu Gly Gln Glu Cys Thr Cys Phe Leu Glu Pro Ala Glu 465 470 475 480			1440
ggt tta gtc ggc gat cat ggc cat gac aac gag gcc tat gag ggt tct Gly Leu Val Gly Asp His Gly His Asp Asn Glu Ala Tyr Glu Gly Ser 485 490 495			1488
gag gtc gac ccg gct gaa cct gca cat ctt gat gtt tct ggg act tac Glu Val Asp Pro Ala Glu Pro Ala His Leu Asp Val Ser Gly Thr Tyr 500 505 510			1536
gcc gtc cac ggg cac cag ctt gag gcc ctc tat agg gca ctt aat gtc Ala Val His Gly His Gln Leu Glu Ala Leu Tyr Arg Ala Leu Asn Val 515 520 525			1584
cca caa gat att gcc gct cga gct tcc cga cta acg gca act gtt gag Pro Gln Asp Ile Ala Ala Arg Ala Ser Arg Leu Thr Ala Thr Val Glu 530 535 540			1632
ctc gtt gca agt cca gac cgc tta gag tgc cgc acc gtg ctc ggt aat Leu Val Ala Ser Pro Asp Arg Leu Glu Cys Arg Thr Val Leu Gly Asn 545 550 555 560			1680
aag acc ttc cgg acg acg gtg gtc gac ggc gcc cat cta gag gcg aat Lys Thr Phe Arg Thr Thr Val Val Asp Gly Ala His Leu Glu Ala Asn 565 570 575			1728
ggc cct gag cag tat gtc tta tca ttt gac gcc tcc cgt cag tct atg Gly Pro Glu Gln Tyr Val Leu Ser Phe Asp Ala Ser Arg Gln Ser Met 580 585 590			1776
ggg gcc ggg tcg cat agc ctc act tat gag ctc acc cct gct ggt ttg Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro Ala Gly Leu 595 600 605			1824
cag gtt agg att tca tct aat ggt ctg gat tgc act gct aca ttc ccc Gln Val Arg Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala Thr Phe Pro 610 615 620			1872
ccc ggt gga gcc cct agc gct gcg ccc ggg gag gtg gca gcc ttt tgc Pro Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Ala Ala Phe Cys 625 630 635 640			1920
agt gcc ctt tat aga tat aac agg ttc acc cag cgg cac tcg ctg act Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His Ser Leu Thr 645 650 655			1968
ggc gga tta tgg tta cac cct gag ggg ttg ctg ggt att ttc ccc cct Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile Phe Pro Pro 660 665 670			2016
ttc tcc cct ggg cat atc tgg gag tct gcg aac ccc ttt tgc ggg gag Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe Cys Gly Glu 675 680 685			2064

ggg act ttg tat acc cga act tgg tca aca tct ggc ttt tct agt gat	2112
Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe Ser Ser Asp	
690 695 700	
ttc tcc ccc cct gaa gcg gcc gct cct gct atg gct gct acc ccg ggg	2160
Phe Ser Pro Pro Glu Ala Ala Ala Pro Ala Met Ala Ala Thr Pro Gly	
705 710 715 720	
ctg ccc cat tct acc cca cct gtt agc gat att tgg gtg cta cca ccg	2208
Leu Pro His Ser Thr Pro Pro Val Ser Asp Ile Trp Val Leu Pro Pro	
725 730 735	
ccc tca gag gag ttt cag gtt gat gca gca cct gtg ccc cct gcc cct	2256
Pro Ser Glu Glu Phe Gln Val Asp Ala Ala Pro Val Pro Pro Ala Pro	
740 745 750	
gac cct gct gga ttg ccc ggt ccc gtt gtg ctt acc ccc ccc ccc cct	2304
Asp Pro Ala Gly Leu Pro Gly Pro Val Val Leu Thr Pro Pro Pro Pro	
755 760 765	
ccc cct gtg cat aag cca tca ata ccc ccg cct tcc cgt aac cgt cgt	2352
Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg	
770 775 780	
ctc ctc tat acc tat cct gac ggc gct aag gtg tat gca ggg tca ctg	2400
Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu	
785 790 795 800	
ttt gaa tca gac tgt gac tgg ctg gtt aat gcc tca aac ccg ggc cat	2448
Phe Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser Asn Pro Gly His	
805 810 815	
cgt ccc gga ggt ggc ctc tgc cat gcc ttt tac caa cgt ttt cca gaa	2496
Arg Pro Gly Gly Glu Leu Cys His Ala Phe Tyr Gln Arg Phe Pro Glu	
820 825 830	
gcg ttt tac cca act gaa ttc atc atg cgt gag ggt ctt gca gca tac	2544
Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr	
835 840 845	
acc ttg acc ccg cgc cct atc att cat gca gtc gct ccc gat tat agg	2592
Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg	
850 855 860	
gtt gag cag aac ccg aag agg ctt gag gca gcg tac cgt gaa act tgt	2640
Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys	
865 870 875 880	
tcc cgt cgt ggc acc gct gcc tac ccg ctt ttg ggt tcg ggt ata tac	2688
Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr	
885 890 895	
cag gtc cct gtt agc ctc agt ttt gat gcc tgg gaa cgt aat cac cgc	2736
Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg	
900 905 910	

ccc ggc gat gag ctt tac ttg acc gag ccc gct gca aat tgg ttt gag	2784
Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala Asn Trp Phe Glu	
915 920 925	
gct aat aag ccg gcg cag ccg gtg ctc acc ata act gag gac acg gcc	2832
Ala Asn Lys Pro Ala Gln Pro Val Leu Thr Ile Thr Glu Asp Thr Ala	
930 935 940	
cgt acg gcc aac ctg gca ttg gag att gat gcc gct aca gag gtc ggc	2880
Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala Thr Glu Val Gly	
945 950 955 960	
cgt gct tgt gcc ggt tgc acc atc agc cct ggc att gtg cac tat cag	2928
Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln	
965 970 975	
ttt acc gcc ggg gtc ccg ggc tcg ggc aag tca agg tcc ata caa cag	2976
Phe Thr Ala Gly Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Gln Gln	
980 985 990	
gga gat gtc gat gtg gtg gtt gtg ccc acc cgg gag ctt cgt aat agt	3024
Gly Asp Val Asp Val Val Val Val Pro Thr Arg Glu Leu Arg Asn Ser	
995 1000 1005	
tgg cgc cgc cgg ggt ttt gcg gcc ttc aca ccc cac aca gcg gcc cgt	3072
Trp Arg Arg Arg Gly Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg	
1010 1015 1020	
gtt act atc ggc cgc cgc gtt gtg att gat gag gct cca tct ctc ccg	3120
Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro	
1025 1030 1035 1040	
cca cac ctg ttg ctg tta cat atg cag cgg gcc tcc tcg gtc cat ctc	3168
Pro His Leu Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu	
1045 1050 1055	
ctc ggt gac cca aat cag atc cct gct att gat ttt gag cac gcc ggc	3216
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly	
1060 1065 1070	
ctg gtc cct gcg atc cgt ccc gag ctt gcg cca acg agc tgg tgg crc	3264
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa	
1075 1080 1085	
gtt aca cac cgt tgc ccg gcc gat gtg tgc gag ctc ata cgc gga gcc	3312
Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala	
1090 1095 1100	
tac cct aaa atc cag acc acg agc cgt gtg cta cgg tcc ctg ttt tgg	3360
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp	
1105 1110 1115 1120	
aat gaa ccg gcc att ggc cag aag ttg gtt ytc acg cag gcg gca aag	3408
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys	
1125 1130 1135	
gct gct aac cct ggt gcg att acg gtc cac gaa gct cag ggt gcc acc	3456

Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr	
1140 1145 1150	
ttc aca gag acc aca atc ata gcc acg gcc gac gcc agg ggc ctt atc	3504
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile	
1155 1160 1165	
cag tca tcc cgg gct cat gct ata gtt gca ctt act cgc cac act gag	3552
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu	
1170 1175 1180	
aag tgt gtt atc ctg gat gcc ccc ggc ctg ctt cgt gag gtc ggc att	3600
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile	
1185 1190 1195 1200	
tcg gat gtg att gtc aac aac ttt ttc ctt gct ggt ggc gag gtc ggc	3648
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly	
1205 1210 1215	
crc cac cgc cct tct gtg ata cct cgc ggt aac cct gat caa aac ctc	3696
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu	
1220 1225 1230	
ggg act tta cag gcc ttc ccg ccg tcc tgt caa att agt gct tac cat	3744
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His	
1235 1240 1245	
cag ttg gct gag gaa ctg ggc cat cgc ccg gcc cct gtc gcc gcc gtc	3792
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val	
1250 1255 1260	
ttg ccc cct tgc cct gag ctt gag cag ggc ctg ctc tac atg cca cag	3840
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln	
1265 1270 1275 1280	
gag ctc act gtg tcc gat agt gtg ttg gtt ttt gag ctt acg gat ata	3888
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile	
1285 1290 1295	
gtt cat tgc cgc atg gcc gct cca agc cag cga aag gct gtt ctc tca	3936
Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser	
1300 1305 1310	
aca ctt gtg ggg agg tat ggc cgt agg acg aaa cta tat gag gcg gcg	3984
Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala	
1315 1320 1325	
cat tca gat gtt cgt gag tcc cta gct agg ttc atc cct act atc ggg	4032
His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly	
1330 1335 1340	
cct gtt cag gct acc aca tgt gag ttg tat gag ttg gtt gag gct atg	4080
Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met	
1345 1350 1355 1360	
gtg gag aaa ggt cag gac ggc tct gca gtc tta gag ctt gat ctt tgt	4128
Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys	

1365	1370	1375	
aat cgt gat gtc tgc cgc atc aca ttt ttc caa aaa gwc tgc aac aag			4176
Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys			
1380	1385	1390	
ttt aca act ggt gag acc atc gcc cac ggc aag gtt ggc cag ggt ata			4224
Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile			
1395	1400	1405	
tgc gcc tgg agt aag acc ttc tgc gct ctg ttc ggc ccg tgg ttc cgc			4272
Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg			
1410	1415	1420	
gcc att gaa aaa gaa ata ttg gcc ctg ctc ccg cct aat atc ttt tat			4320
Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr			
1425	1430	1435	1440
ggc gac gct tat gag gag tca gtt ttt gcc gcc gct gtg tcc ggg gcg			4368
Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala Val Ser Gly Ala			
1445	1450	1455	
ggg tca tgt atg gta ttt gaa aat gac ttt tca gag ttt gac agt acc			4416
Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr			
1460	1465	1470	
cag aat aat ttc tct ctt ggc ctt gag tgt gtg gtt atg gag gag tgc			4464
Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys			
1475	1480	1485	
ggc atg cct caa tgg cta att agg ttg tac cat ctg gtt cgg tct gcc			4512
Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Val Arg Ser Ala			
1490	1495	1500	
tgg att ctg cag gcg ccg aag gag tct ctt aag ggt ttc tgg aag aag			4560
Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys			
1505	1510	1515	1520
cat tct ggt gag cct ggt acc ctt ctt tgg aat acc gtc tgg aat atg			4608
His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met			
1525	1530	1535	
gcg att ata gca cat tgc tat gag ttc cgt gac ttt cgt gtt gct gcc			4656
Ala Ile Ile Ala His Cys Tyr Glu Phe Arg Asp Phe Arg Val Ala Ala			
1540	1545	1550	
ttt aag ggt gat gat tgc gtg gtc ctc tgt agt gac tac cga cag agc			4704
Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp Tyr Arg Gln Ser			
1555	1560	1565	
cgc aat gca gct gcc tta att gct ggc tgt ggg ctc aaa ttg aag gtt			4752
Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val			
1570	1575	1580	
gat tac cgc cct atc ggg ctg tat gct ggg gtg gtg gtg gcc ccc ggt			4800
Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly			
1585	1590	1595	1600

ttg ggg aca ctg ccc gat gtg gtg cgt ttt gct ggt cgg ttg tct gaa	4848
Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu	
1605 1610 1615	
aag aat tgg ggc ccc ggc ccg gaa cgt gct gag cag ctg cgt ctt gct	4896
Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala	
1620 1625 1630	
gtc tgc gac ttc ctt cga ggg ttg acg aat gtt gcg cag gtc tgt gtt	4944
Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val	
1635 1640 1645	
gat gtt gtg tcc cgt gtc tat gga gtc agc ccc ggg ctc gta cat aac	4992
Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn	
1650 1655 1660	
ctt att ggc atg ctg cag acc atc gcc gat ggc aag gcc cac ttt aca	5040
Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr	
1665 1670 1675 1680	
gag act att aaa cct gta ctt gat ctc aca aat tcc atc ata cag cgg	5088
Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg	
1685 1690 1695	
gtg gaa tga ataacatgtc ttttgcacgc cccatgggat cacc atg cgc cct agg	5143
Val Glu Met Arg Pro Arg	
1700	
gct gtt ctg ttg ttg ttc ctc atg ttt ctg cct atg ctg ccc gcg cca	5191
Ala Val Leu Leu Leu Phe Leu Met Phe Leu Pro Met Leu Pro Ala Pro	
1705 1710 1715	
ccg gcc ggt cag ccg tct ggc cgt cgc cgt ggg cgg cgc agc ggc ggt	5239
Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly	
1720 1725 1730 1735	
gcc ggc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc	5287
Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala	
1740 1745 1750	
ctc ccc tat att cat cca acc aac ccc ttc gcc gcc gat gtc gtt tca	5335
Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser	
1755 1760 1765	
caa ccc ggg gct gga act cgc cct cga cag ccg ccc cgc ccc ctc ggt	5383
Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly	
1770 1775 1780	
tcc gct tgg cgt gac cag tcc aag cgc ccc tcc gtt gcc ccc cgt cgt	5431
Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val Ala Pro Arg Arg	
1785 1790 1795	
cga tct acc cca gct ggg gct gcg ccg cta act gcc ata tca cca gcc	5479
Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Ile Ser Pro Ala	
1800 1805 1810 1815	

cct gat aca gct cct gta cct gat gtt gac tca cgt ggt gct att ttg	5527
Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu	
1820 1825 1830	
cgc cgg cag tac aat ttg tct acg tcc ccg ctt aca tca tct gtt gct	5575
Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala	
1835 1840 1845	
tct ggt act aat ctg gtt ctc tat gct gcc ccg ctg aac cct ctc ttg	5623
Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Asn Pro Leu Leu	
1850 1855 1860	
cct ctt cag gat ggc acc aac act cat att atg gct act gag gca tct	5671
Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser	
1865 1870 1875	
aat tac gcc cag tat cgg gtt gtt cgg gct acg att cgt tat cgc ccg	5719
Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile Arg Tyr Arg Pro	
1880 1885 1890 1895	
ttg gtg cca aat gct gtt ggt ggt tat gct atc tct att tct ttc tgg	5767
Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser Phe Trp	
1900 1905 1910	
cct caa act aca act acc cct act tct gtt gac atg aat tct atc act	5815
Pro Gln Thr Thr Thr Pro Thr Ser Val Asp Met Asn Ser Ile Thr	
1915 1920 1925	
tct act gat gtc agg atc ttg gtc cag ccc ggt ata gcc tcc gag tta	5863
Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile Ala Ser Glu Leu	
1930 1935 1940	
gtc atc cct agt gaa cgc ctt cac tac cgc aac caa ggc tgg cgc tct	5911
Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln Gly Trp Arg Ser	
1945 1950 1955	
gtt gag acc acg ggt gtg gcc gaa gag gag gct acc tcc ggt ctg gta	5959
Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr Ser Gly Leu Val	
1960 1965 1970 1975	
atg ctt tgt att cat ggc tcc cct gtt aac tcc tac act aat aca cct	6007
Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro	
1980 1985 1990	
tac acc ggt gca ttg ggg ctt ctt gat ttt gca tta gaa ctt gaa ttt	6055
Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe	
1995 2000 2005	
aga aat ttg aca ccc ggg aac act aac acc cgt gtt tcc cgg tat act	6103
Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val Ser Arg Tyr Thr	
2010 2015 2020	
agc aca gcc cgc cac cgg ctg cgc cgc ggt gct gat ggg acc gct gag	6151
Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu	
2025 2030 2035	
ctc acc acc aca gca gcc aca cgc ttc atg aag gat ttg cat ttt act	6199

Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr	
2040	2045 2050 2055
ggt acg aac ggc gtt ggt gag gtg ggt cgt ggt att gcc ctg act ctg	6247
Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu	
2060	2065 2070
ttt aat ctt gct gat acg ctt ctt ggt ggt tta ccg aca gaa ttg att	6295
Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile	
2075	2080 2085
tcg tcg gct ggg ggt caa ctg ttt tac tcc cgc cct gtt gtc tcg gcc	6343
Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala	
2090	2095 2100
aat ggc gag cca aca gta aag tta tac aca tct gtt gag aat gcg cag	6391
Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln	
2105	2110 2115
caa gac aag ggc atc acc att cca cac gac ata gat tta ggt gac tcc	6439
Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu Gly Asp Ser	
2120	2125 2130 2135
cgt gtg gtt atc cag gat tat gat aac cag cac gaa caa gat cga cct	6487
Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro	
2140	2145 2150
acc ccg tca cct gcc ccc tcc cgc cct ttc tca gtt ctt cgt gcc aat	6535
Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn	
2155	2160 2165
gat gtt ttg tgg ctg tct ctc act gcc gct gag tac grc cag acc acg	6583
Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Xaa Gln Thr Thr	
2170	2175 2180
tat ggg tcg tcc acc aac cct atg tat gtc tct gat aca gtc acg ctt	6631
Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Leu	
2185	2190 2195
ggt aat gta gcc act ggt gct cag gct gtt gcc cgc tct ctt gac tgg	6679
Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser Leu Asp Trp	
2200	2205 2210 2215
tct aaa gtt act ctg gat ggt cgc cct ctt act acc att cag cag tat	6727
Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr	
2220	2225 2230
tct aag aaa ttt tat gtt ctg ccg ctt cgs ggg aag ctg tcc ttt tgg	6775
Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys Leu Ser Phe Trp	
2235	2240 2245
gag gct ggt acg acc aag gcc ggc tac ccg tat aat tat aat acc act	6823
Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr	
2250	2255 2260
gct agt gac caa att ttg att gag aac gcg gcc ggt cac cgt gtc gcc	6871
Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala	

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Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
                20                               25                               30
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
          35                               40                               45
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
  50                               55                               60
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
  65                               70                               75                               80
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
                85                               90                               95
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
          100                               105                               110
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly

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115					120					125					
Leu	Pro	Pro	Ala	Asp	Arg	Thr	Tyr	Cys	Phe	Asp	Gly	Phe	Ser	Arg	Cys
130						135					140				
Ala	Phe	Ala	Ala	Glu	Thr	Gly	Val	Ala	Leu	Tyr	Ser	Leu	His	Asp	Leu
145					150					155					160
Trp	Pro	Ala	Asp	Val	Ala	Glu	Ala	Met	Ala	Arg	His	Gly	Xaa	Thr	Arg
				165					170					175	
Leu	Tyr	Ala	Ala	Leu	His	Leu	Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly
			180					185					190		
Thr	Tyr	His	Thr	Thr	Ser	Tyr	Leu	Leu	Ile	His	Asp	Gly	Asp	Arg	Ala
		195					200					205			
Val	Val	Thr	Tyr	Glu	Gly	Asp	Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val
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Ser	Ile	Leu	Arg	Ala	Trp	Ile	Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His
225					230					235					240
Pro	Leu	Val	Ile	Glu	Arg	Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu
				245					250					255	
Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr
			260					265					270		
Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly
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Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His
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Ala	Val	Pro	Val	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr
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Leu	Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg
				325					330					335	
Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly
		340						345					350		
Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Xaa	Ile	Thr	Ala	Ala	Tyr
	355						360					365			
Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys
	370					375					380				
Gly	Met	Arg	Arg	Leu	Gly	Val	Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg
385					390					395					400
Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly
				405					410					415	
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly

420										425					430				
Phe	His	Leu	Asp	Pro	Arg	Val	Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys				
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Arg	Cys	Arg	Thr	Phe	Leu	Lys	Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe				
	450					455					460								
Met	Arg	Trp	Leu	Gly	Gln	Glu	Cys	Thr	Cys	Phe	Leu	Glu	Pro	Ala	Glu				
465					470					475					480				
Gly	Leu	Val	Gly	Asp	His	Gly	His	Asp	Asn	Glu	Ala	Tyr	Glu	Gly	Ser				
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Glu	Val	Asp	Pro	Ala	Glu	Pro	Ala	His	Leu	Asp	Val	Ser	Gly	Thr	Tyr				
			500					505					510						
Ala	Val	His	Gly	His	Gln	Leu	Glu	Ala	Leu	Tyr	Arg	Ala	Leu	Asn	Val				
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Pro	Gln	Asp	Ile	Ala	Ala	Arg	Ala	Ser	Arg	Leu	Thr	Ala	Thr	Val	Glu				
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Leu	Val	Ala	Ser	Pro	Asp	Arg	Leu	Glu	Cys	Arg	Thr	Val	Leu	Gly	Asn				
545					550				555						560				
Lys	Thr	Phe	Arg	Thr	Thr	Val	Val	Asp	Gly	Ala	His	Leu	Glu	Ala	Asn				
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Gly	Pro	Glu	Gln	Tyr	Val	Leu	Ser	Phe	Asp	Ala	Ser	Arg	Gln	Ser	Met				
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Gly	Ala	Gly	Ser	His	Ser	Leu	Thr	Tyr	Glu	Leu	Thr	Pro	Ala	Gly	Leu				
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Gln	Val	Arg	Ile	Ser	Ser	Asn	Gly	Leu	Asp	Cys	Thr	Ala	Thr	Phe	Pro				
	610					615					620								
Pro	Gly	Gly	Ala	Pro	Ser	Ala	Ala	Pro	Gly	Glu	Val	Ala	Ala	Phe	Cys				
625					630					635					640				
Ser	Ala	Leu	Tyr	Arg	Tyr	Asn	Arg	Phe	Thr	Gln	Arg	His	Ser	Leu	Thr				
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Gly	Gly	Leu	Trp	Leu	His	Pro	Glu	Gly	Leu	Leu	Gly	Ile	Phe	Pro	Pro				
		660						665					670						
Phe	Ser	Pro	Gly	His	Ile	Trp	Glu	Ser	Ala	Asn	Pro	Phe	Cys	Gly	Glu				
		675					680					685							
Gly	Thr	Leu	Tyr	Thr	Arg	Thr	Trp	Ser	Thr	Ser	Gly	Phe	Ser	Ser	Asp				
	690					695					700								
Phe	Ser	Pro	Pro	Glu	Ala	Ala	Ala	Pro	Ala	Met	Ala	Ala	Thr	Pro	Gly				
705					710					715					720				
Leu	Pro	His	Ser	Thr	Pro	Pro	Val	Ser	Asp	Ile	Trp	Val	Leu	Pro	Pro				

725										730					735				
Pro	Ser	Glu	Glu	Phe	Gln	Val	Asp	Ala	Ala	Pro	Val	Pro	Pro	Ala	Pro				
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Asp	Pro	Ala	Gly	Leu	Pro	Gly	Pro	Val	Val	Leu	Thr	Pro	Pro	Pro	Pro				
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Pro	Pro	Val	His	Lys	Pro	Ser	Ile	Pro	Pro	Pro	Ser	Arg	Asn	Arg	Arg				
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Leu	Leu	Tyr	Thr	Tyr	Pro	Asp	Gly	Ala	Lys	Val	Tyr	Ala	Gly	Ser	Leu				
785					790					795					800				
Phe	Glu	Ser	Asp	Cys	Asp	Trp	Leu	Val	Asn	Ala	Ser	Asn	Pro	Gly	His				
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Arg	Pro	Gly	Gly	Gly	Leu	Cys	His	Ala	Phe	Tyr	Gln	Arg	Phe	Pro	Glu				
			820					825					830						
Ala	Phe	Tyr	Pro	Thr	Glu	Phe	Ile	Met	Arg	Glu	Gly	Leu	Ala	Ala	Tyr				
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Thr	Leu	Thr	Pro	Arg	Pro	Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg				
	850					855					860								
Val	Glu	Gln	Asn	Pro	Lys	Arg	Leu	Glu	Ala	Ala	Tyr	Arg	Glu	Thr	Cys				
865					870						875				880				
Ser	Arg	Arg	Gly	Thr	Ala	Ala	Tyr	Pro	Leu	Leu	Gly	Ser	Gly	Ile	Tyr				
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Gln	Val	Pro	Val	Ser	Leu	Ser	Phe	Asp	Ala	Trp	Glu	Arg	Asn	His	Arg				
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Pro	Gly	Asp	Glu	Leu	Tyr	Leu	Thr	Glu	Pro	Ala	Ala	Asn	Trp	Phe	Glu				
		915					920					925							
Ala	Asn	Lys	Pro	Ala	Gln	Pro	Val	Leu	Thr	Ile	Thr	Glu	Asp	Thr	Ala				
	930					935					940								
Arg	Thr	Ala	Asn	Leu	Ala	Leu	Glu	Ile	Asp	Ala	Ala	Thr	Glu	Val	Gly				
945				950					955						960				
Arg	Ala	Cys	Ala	Gly	Cys	Thr	Ile	Ser	Pro	Gly	Ile	Val	His	Tyr	Gln				
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Phe	Thr	Ala	Gly	Val	Pro	Gly	Ser	Gly	Lys	Ser	Arg	Ser	Ile	Gln	Gln				
			980					985					990						
Gly	Asp	Val	Asp	Val	Val	Val	Val	Pro	Thr	Arg	Glu	Leu	Arg	Asn	Ser				
		995					1000					1005							
Trp	Arg	Arg	Arg	Gly	Phe	Ala	Ala	Phe	Thr	Pro	His	Thr	Ala	Ala	Arg				
	1010				1015						1020								
Val	Thr	Ile	Gly	Arg	Arg	Val	Val	Ile	Asp	Glu	Ala	Pro	Ser	Leu	Pro				

025	1030	1035	1040
Pro His Leu Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu	1045	1050	1055
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly	1060	1065	1070
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa	1075	1080	1085
Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala	1090	1095	1100
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp	1105	1110	1115
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys	1125	1130	1135
Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr	1140	1145	1150
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile	1155	1160	1165
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu	1170	1175	1180
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile	1185	1190	1195
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly	1205	1210	1215
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu	1220	1225	1230
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His	1235	1240	1245
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val	1250	1255	1260
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln	1265	1270	1275
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile	1285	1290	1295
Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser	1300	1305	1310
Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala	1315	1320	1325
His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly			

1330	1335	1340
Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met 345	1350	1355 1360
Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys 1365	1370	1375
Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys 1380	1385	1390
Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile 1395	1400	1405
Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg 1410	1415	1420
Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr 425	1430	1435 1440
Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala Val Ser Gly Ala 1445	1450	1455
Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr 1460	1465	1470
Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys 1475	1480	1485
Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Val Arg Ser Ala 1490	1495	1500
Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys 505	1510	1515 1520
His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met 1525	1530	1535
Ala Ile Ile Ala His Cys Tyr Glu Phe Arg Asp Phe Arg Val Ala Ala 1540	1545	1550
Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp Tyr Arg Gln Ser 1555	1560	1565
Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val 1570	1575	1580
Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly 585	1590	1595 1600
Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu 1605	1610	1615
Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala 1620	1625	1630
Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val		

1635 1640 1645
 Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn
 1650 1655 1660
 Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr
 665 1670 1675 1680
 Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg
 1685 1690 1695
 Val Glu

<210> 92

<211> 660

<212> PRT

<213> Hepatitis E virus

<400> 92

 Met Arg Pro Arg Ala Val Leu Leu Leu Phe Leu Met Phe
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 Leu Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg
 15 20 25
 Arg Gly Arg Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Ser Asp Arg
 30 35 40 45
 Val Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro
 50 55 60
 Phe Ala Ala Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg
 65 70 75
 Gln Pro Pro Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Lys Arg
 80 85 90
 Pro Ser Val Ala Pro Arg Arg Arg Ser Thr Pro Ala Gly Ala Ala Pro
 95 100 105
 Leu Thr Ala Ile Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val
 10 115 120 125
 Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser
 130 135 140
 Pro Leu Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala
 145 150 155
 Ala Pro Leu Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His
 160 165 170
 Ile Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg
 175 180 185
 Ala Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr

90	195	200	205
Ala Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser	210	215	220
Val Asp Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln	225	230	235
Pro Gly Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr	240	245	250
Arg Asn Gln Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu	255	260	265
Glu Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val	270	275	280
Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp	290	295	300
Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn	305	310	315
Thr Arg Val Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg	320	325	330
Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe	335	340	345
Met Lys Asp Leu His Phe Thr Gly Thr Asn Gly Val Gly Glu Val Gly	350	355	360
Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly	370	375	380
Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr	385	390	395
Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr	400	405	410
Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His	415	420	425
Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn	430	435	440
Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro	450	455	460
Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala	465	470	475
Ala Glu Tyr Xaa Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr	480	485	490
Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala			

495 500 505
 Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro
 10 515 520 525
 Leu Thr Thr Ile Gln Gln Tyr Ser Lys Lys Phe Tyr Val Leu Pro Leu
 530 535 540
 Xaa Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr
 545 550 555
 Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn
 560 565 570
 Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly
 575 580 585
 Ala Gly Pro Thr Ser Xaa Ser Ala Val Gly Val Leu Ala Pro His Ser
 90 595 600 605
 Ala Leu Ala Val Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His
 610 615 620
 Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly
 625 630 635
 Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys
 640 645 650
 Val Gly Lys Thr Arg Glu Ser
 655 660

 <210> 93
 <211> 122
 <212> PRT
 <213> Hepatitis E virus

 <220>
 <223> ORF3 HEV US-1

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 Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
 20 25 30
 His Arg Pro Val Ser Arg Leu Ala Val Ala Val Gly Gly Ala Ala Ala
 35 40 45
 Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
 50 55 60
 Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser Phe
 65 70 75 80

His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser
 85 90 95

Val Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro Pro Val
 100 105 110

Val Asp Leu Pro Gln Leu Gly Leu Arg Arg
 115 120

<210> 94
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 US5P3S/20

<400> 94
 tggcattact actgccattg 20

<210> 95
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 US5P45S/20

<400> 95
 caattctgcc ttggcgaatg 20

<210> 96
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 US5P296A

<400> 96
 aggaaacacc gatgcagaac 20

<210> 97
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 US5P243A/20

<400> 97
tccaacctcc aagcaacgac

20

<210> 98
<211> 199
<212> DNA
<213> Hepatitis E virus

<220>
<223> Clone 199con

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tcacacctatc cagcgggtta tacataatga attagagcag tactgccggg cccgggctgg 180
tcgttgcttg gaggttgga 199

<210> 99
<211> 25
<212> DNA
<213> Hepatitis E virus

<220>
<223> JE orf1-s

<400> 99
gttctgcatc ggtgttctct tagac 25

<210> 100
<211> 26
<212> DNA
<213> Hepatitis E virus

<220>
<223> JE orf1-a

<400> 100
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<210> 101
<211> 331
<212> DNA
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<220>
<223> us2-320

<400> 101
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 gaccgcacct attgttttga tggattttcc cgttgtgctt ttgctgcaga gaccgggtgtg 180
 gccctttact ctttgcata cctttggcca gctgatgttg cagaggctat ggcccggcat 240
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 acctaccaca caacctcgta tctcctgatt c 331

<210> 102
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 <212> DNA
 <213> Hepatitis E virus

<220>
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<223> JE hev167-a1

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<211> 580

<212> DNA

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<223> us2-579

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Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	
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gtt	ccc	tac	cct	cgt	tca	acg	gag	gtg	tat	gtc	cgg	tct	ata	ttt	ggc	917
Val	Pro	Tyr	Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	
	280					285				290						
cct	ggc	ggc	tcc	cca	tcc	ttg	ttt	cca	tca	gcc	tgc	tct	act	aaa	tct	965
Pro	Gly	Gly	Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	
295					300					305					310	
acc	ttt	cat	gct	gtc	ccg	gtt	cac	atc	tgg	gat	crg	ctc	atg	ctc	ttt	1013
Thr	Phe	His	Ala	Val	Pro	Val	His	Ile	Trp	Asp	Xaa	Leu	Met	Leu	Phe	
			315						320					325		
ggg	gcc	acc	ctg	rac	gat	cag	gcg	ttc	tgc	tgt	tca	cgg	ctt	atg	act	1061
Gly	Ala	Thr	Leu	Xaa	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	
			330					335					340			
tac	ctc	cgt	ggg	att	agt	tat	aag	gtc	act	gtc	ggg	gcg	ctt	gtc	gct	1109
Tyr	Leu	Arg	Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	
		345					350					355				
aat	gag	ggg	tgg	aac	gcc	tct	gag	gat	gct	ctt	act	gca	gtg	atc	act	1157
Asn	Glu	Gly	Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Val	Ile	Thr	
	360					365					370					
gcg	gcc	tat	ctg	acc	atc	tgc	cat	cag	cgt	tac	ctt	cgc	acc	cag	gcg	1205
Ala	Ala	Tyr	Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	
375					380					385					390	
att	tcc	aag	ggc	atg	cgc	cgg	ttg	gag	gtt	gag	cat	gct	cag	aaa	ttt	1253
Ile	Ser	Lys	Gly	Met	Arg	Arg	Leu	Glu	Val	Glu	His	Ala	Gln	Lys	Phe	
				395				400						405		
atc	aca	aga	ctc	tac	agc	tgg	cta	ttt	gag	aag	tct	ggc	cgt	gac	tac	1301
Ile	Thr	Arg	Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	
			410					415					420			
atc	ccc	ggc	cgc	cag	ctt	caa	ttt	tat	gca	caa	tgc	cga	cgg	tgg	ctt	1349
Ile	Pro	Gly	Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	
	425					430						435				
tct	gca	ggc	ttc	cac	cta	rac	ccc	agg	rtg	ctt	gtc	ttt	gat	gaa	tca	1397
Ser	Ala	Gly	Phe	His	Leu	Xaa	Pro	Arg	Xaa	Leu	Val	Phe	Asp	Glu	Ser	
	440					445					450					
gtg	cca	tgc	cgt	tgc	agg	acg	ttt	ttg	aag	aag	gtc	gcg	ggg	aaa	ttc	1445
Val	Pro	Cys	Arg	Cys	Arg	Thr	Phe	Leu	Lys	Lys	Val	Ala	Gly	Lys	Phe	
455					460					465					470	
tgc	tgt	ttt	atg	cgg	tgg	ctg	ggg	cag	gag	tgt	acc	tgc	ttc	ttg	gag	1493
Cys	Cys	Phe	Met	Arg	Trp	Leu	Gly	Gln	Glu	Cys	Thr	Cys	Phe	Leu	Glu	
				475					480					485		

cca gcc gag ggt tta gtt ggt gat caa ggt cat gac aac gag gcc tat	1541
Pro Ala Glu Gly Leu Val Gly Asp Gln Gly His Asp Asn Glu Ala Tyr	
490 495 500	
gaa ggt tct gag gtc gac cca gct gag cct gca cat ctt gat gtc tcg	1589
Glu Gly Ser Glu Val Asp Pro Ala Glu Pro Ala His Leu Asp Val Ser	
505 510 515	
ggg act tat gcc gtc cat ggg cac cag ctt gag gcc ctc tat agg gca	1637
Gly Thr Tyr Ala Val His Gly His Gln Leu Glu Ala Leu Tyr Arg Ala	
520 525 530	
ctt aat gtc cca cat gat att gcc gct cga gcc tcc cga cta acg gct	1685
Leu Asn Val Pro His Asp Ile Ala Ala Arg Ala Ser Arg Leu Thr Ala	
535 540 545 550	
act gtt gag ctc gtt gct agt ccg gac cgc tta gag tgc cgc act gta	1733
Thr Val Glu Leu Val Ala Ser Pro Asp Arg Leu Glu Cys Arg Thr Val	
555 560 565	
ctt ggt aat aag acc ttc cgg acg acg gtg gtt gat ggc gcc cat ctt	1781
Leu Gly Asn Lys Thr Phe Arg Thr Thr Val Val Asp Gly Ala His Leu	
570 575 580	
gaa gcg aat ggc cct gag gag tat gtt ctg tca ttt gac gcc tct cgc	1829
Glu Ala Asn Gly Pro Glu Glu Tyr Val Leu Ser Phe Asp Ala Ser Arg	
585 590 595	
cag tct atg ggg gcc ggg tcg cac agc ctc act tat gag ctc acc cct	1877
Gln Ser Met Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro	
600 605 610	
gcc ggt ctg cag gta aag att tca tct aat ggt ctg gat tgc act gcc	1925
Ala Gly Leu Gln Val Lys Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala	
615 620 625 630	
aca ttc ccc ccg ggt ggc gcc cct agc gcc gcg ccg ggg gag gtg gcs	1973
Thr Phe Pro Xaa Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Xaa	
635 640 645	
gcc ttc tgc agt gct ctt tat aga tac aat agg ttc acc cag cgg cat	2021
Ala Phe Cys Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His	
650 655 660	
tcg ctg aca ggc gga cta tgg cta cat cct gag ggg ctg ctg ggt atc	2069
Ser Leu Thr Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile	
665 670 675	
ttc ccc cca ttc tcc cct ggg cat att tgg gag tct gct aac ccc ttt	2117
Phe Pro Pro Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe	
680 685 690	
tgc ggt gag ggg act ttg tat acc cga acc tgg tca acc tct ggt ttt	2165
Cys Gly Glu Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe	
695 700 705 710	
tct agt gat ttc tcc ccc cct gag gcg gcc gct cct gct tcg gct gcc	2213

Ser	Ser	Asp	Phe	Ser	Pro	Pro	Glu	Ala	Ala	Ala	Pro	Ala	Ser	Ala	Ala		
				715					720					725			
gcc	ccg	ggg	tgg	ccc	tac	cct	act	cca	cct	gtt	agt	gat	atc	tgg	gtg	2261	
Ala	Pro	Gly	Leu	Pro	Tyr	Pro	Thr	Pro	Pro	Val	Ser	Asp	Ile	Trp	Val		
			730					735					740				
tta	cca	ccg	ccc	tca	gag	gaa	tct	cat	gtt	gat	gcg	gca	tct	gta	ccc	2309	
Leu	Pro	Pro	Pro	Ser	Glu	Glu	Ser	His	Val	Asp	Ala	Ala	Ser	Val	Pro		
			745				750					755					
tct	gtt	cct	gag	cct	gct	gga	ttg	acc	agc	cct	att	gtg	ctt	acc	ccc	2357	
Ser	Val	Pro	Glu	Pro	Ala	Gly	Leu	Thr	Ser	Pro	Ile	Val	Leu	Thr	Pro		
	760					765					770						
ccc	ccc	ccc	cct	cct	ccc	gtg	cgt	aag	ccg	gca	aca	tcc	ccg	cct	ccc	2405	
Pro	Pro	Pro	Pro	Pro	Pro	Val	Arg	Lys	Pro	Ala	Thr	Ser	Pro	Pro	Pro		
	775				780					785					790		
cgc	act	cgc	cgt	ctc	ctt	tac	acc	tac	ccc	gac	ggc	gcc	aag	gtg	tat	2453	
Arg	Thr	Arg	Arg	Leu	Leu	Tyr	Thr	Tyr	Pro	Asp	Gly	Ala	Lys	Val	Tyr		
				795					800					805			
gcg	ggg	tca	ttg	tkt	gag	tca	gac	tgt	gat	tgg	tta	gtc	aat	gcc	tca	2501	
Ala	Gly	Ser	Leu	Xaa	Glu	Ser	Asp	Cys	Asp	Trp	Leu	Val	Asn	Ala	Ser		
			810				815						820				
aac	cct	ggc	cat	cgc	ccc	ggg	ggt	ggc	ctc	tgc	cat	gct	ttt	tat	caa	2549	
Asn	Pro	Gly	His	Arg	Pro	Gly	Gly	Gly	Leu	Cys	His	Ala	Phe	Tyr	Gln		
		825					830					835					
cgt	ttc	cca	gaa	gcg	ttc	tac	tgc	act	gaa	ttc	atc	atg	cgc	gag	ggc	2597	
Arg	Phe	Pro	Glu	Ala	Phe	Tyr	Ser	Thr	Glu	Phe	Ile	Met	Arg	Glu	Gly		
	840					845					850						
ctt	gca	gca	tac	act	tta	acc	ccg	cgc	cct	att	atc	cat	gca	gtg	gct	2645	
Leu	Ala	Ala	Tyr	Thr	Leu	Thr	Pro	Arg	Pro	Ile	Ile	His	Ala	Val	Ala		
	855				860					865					870		
ccc	gac	tat	agg	gtt	gag	caa	aac	ccg	aag	agg	ctt	gag	gca	gcg	tac	2693	
Pro	Asp	Tyr	Arg	Val	Glu	Gln	Asn	Pro	Lys	Arg	Leu	Glu	Ala	Ala	Tyr		
			875					880					885				
cgg	gaa	act	tgc	tcc	cgt	cgt	ggc	acc	gct	gcc	tac	ccg	ctt	ttg	ggc	2741	
Arg	Glu	Thr	Cys	Ser	Arg	Arg	Gly	Thr	Ala	Ala	Tyr	Pro	Leu	Leu	Gly		
			890				895						900				
tgc	ggt	ata	tac	cag	gtc	cct	gtt	agc	ctc	agt	ttt	gat	gcc	tgg	gaa	2789	
Ser	Gly	Ile	Tyr	Gln	Val	Pro	Val	Ser	Leu	Ser	Phe	Asp	Ala	Trp	Glu		
		905				910					915						
cgc	aat	cac	cgc	ccc	ggc	gat	gag	ctt	tac	ttg	aca	gag	ccc	gcc	gca	2837	
Arg	Asn	His	Arg	Pro	Gly	Asp	Glu	Leu	Tyr	Leu	Thr	Glu	Pro	Ala	Ala		
	920					925					930						
gcc	tgg	ttt	gag	gct	aat	aag	ccg	gcg	cag	ccg	gcg	ctt	act	ata	act	2885	
Ala	Trp	Phe	Glu	Ala	Asn	Lys	Pro	Ala	Gln	Pro	Ala	Leu	Thr	Ile	Thr		

935	940	945	950	
gag gac acg gcc cgt	acg gcc aac ctg	gca tta gag att	gat gcc gcc	2933
Glu Asp Thr Ala Arg	Thr Ala Asn Leu	Ala Leu Glu Ile	Asp Ala Ala	
	955	960	965	
aca gag gtt ggc cgt gct tgt	gcc ggc tgc acc atc	agc ccc ggg att		2981
Thr Glu Val Gly Arg Ala Cys	Ala Gly Cys Thr Ile	Ser Pro Gly Ile		
	970	975	980	
gtg cac tat cag ttt acc gcc ggg gtc	ccg ggc tca ggc aag tca agg			3029
Val His Tyr Gln Phe Thr Ala Gly Val	Pro Gly Ser Gly Lys Ser Arg			
	985	990	995	
tcc ata caa cag gga gat gtc	gat gtg gtg gtt gtg	ccc acc cgg gag		3077
Ser Ile Gln Gln Gly Asp Val	Asp Val Val Val Val	Pro Thr Arg Glu		
	1000	1005	1010	
ctc cgt aac agc tgg cgt cgc	cgg ggt ttt gcg gcc ttc	aca cct cac		3125
Leu Arg Asn Ser Trp Arg Arg	Arg Gly Phe Ala Ala	Phe Thr Pro His		
	1015	1020	1025	1030
aca gcg gcc cgt gtt act atc	ggc cgc cgc gtt gtg att	gat gag gct		3173
Thr Ala Ala Arg Val Thr Ile	Gly Arg Arg Val Val	Ile Asp Glu Ala		
	1035	1040	1045	
cca tct ctc cca ccg cac ctg	ctg ctg tta cac atg	cag cgg gcc tcc		3221
Pro Ser Leu Pro Pro His Leu	Leu Leu Leu His Met	Gln Arg Ala Ser		
	1050	1055	1060	
tcg gtc cat ctc ctt ggt gat	cca aac cag att cct	gct att gat ttt		3269
Ser Val His Leu Leu Gly Asp	Pro Asn Gln Ile Pro	Ala Ile Asp Phe		
	1065	1070	1075	
gag cat gcc ggc ctg gtc ccc	gcg atc cgc ccc gag	ctt gcg cca acg		3317
Glu His Ala Gly Leu Val Pro	Ala Ile Arg Pro Glu	Leu Ala Pro Thr		
	1080	1085	1090	
agc tgg tgg cac gtt aca cac	cgt tgc ccg gcc gat	gtg tgc gag ctc		3365
Ser Trp Trp His Val Thr His	Arg Cys Pro Ala Asp	Val Cys Glu Leu		
	1095	1100	1105	1110
ata cgt ggg gcc tac ccc aaa	att cag acc acg agc	cgt gtg cta cgg		3413
Ile Arg Gly Ala Tyr Pro Lys	Ile Gln Thr Thr Ser	Arg Val Leu Arg		
	1115	1120	1125	
tcc ctg ttt tgg aac gaa ccg	gcc atc ggc caa aag	ttg gtt ttt acg		3461
Ser Leu Phe Trp Asn Glu Pro	Ala Ile Gly Gln Lys	Leu Val Phe Thr		
	1130	1135	1140	
cag gct gct aag gct gcc aac	cct ggt gcg att acg	ggt cac gaa gct		3509
Gln Ala Ala Lys Ala Ala Asn	Pro Gly Ala Ile Thr	Val His Glu Ala		
	1145	1150	1155	
cag ggt gct act ttc acg gag	acc aca att ata gcc	acg gcc gac gct		3557
Gln Gly Ala Thr Phe Thr Glu	Thr Thr Ile Ile Ala	Thr Ala Asp Ala		
	1160	1165	1170	

agg	ggc	ctc	att	cag	tca	tcc	cgg	gcc	cat	gct	ata	gtc	gca	ctc	acc	3605
Arg	Gly	Leu	Ile	Gln	Ser	Ser	Arg	Ala	His	Ala	Ile	Val	Ala	Leu	Thr	
1175				1180						1185					1190	
cgc	cat	act	gag	aag	tgt	gtt	att	ttg	gat	gcc	ccc	ggc	ttg	ttg	cgc	3653
Arg	His	Thr	Glu	Lys	Cys	Val	Ile	Leu	Asp	Ala	Pro	Gly	Leu	Leu	Arg	
			1195					1200					1205			
gag	gtc	ggc	att	tcg	gat	gtt	att	gtc	aat	aac	ttt	ttc	ctt	gcc	ggc	3701
Glu	Val	Gly	Ile	Ser	Asp	Val	Ile	Val	Asn	Asn	Phe	Phe	Leu	Ala	Gly	
		1210					1215					1220				
gga	gag	gtc	ggc	cat	cac	cgc	cct	tct	gtg	ata	cct	cgc	ggc	aat	cct	3749
Gly	Glu	Val	Gly	His	His	Arg	Pro	Ser	Val	Ile	Pro	Arg	Gly	Asn	Pro	
	1225					1230					1235					
gat	cag	aac	ctc	ggg	act	cta	cag	gcc	ttt	ccg	ccg	tca	tgt	cag	atc	3797
Asp	Gln	Asn	Leu	Gly	Thr	Leu	Gln	Ala	Phe	Pro	Pro	Ser	Cys	Gln	Ile	
1240				1245						1250						
agt	gct	tac	cat	cag	ttg	gct	gag	gaa	cta	ggc	cat	cgc	ccg	gcc	cct	3845
Ser	Ala	Tyr	His	Gln	Leu	Ala	Glu	Glu	Leu	Gly	His	Arg	Pro	Ala	Pro	
1255			1260					1265						1270		
gtc	gcc	gcc	gtc	ttg	ccc	cct	tgc	cct	gag	ctt	gag	cag	ggc	ctg	ctc	3893
Val	Ala	Ala	Val	Leu	Pro	Pro	Cys	Pro	Glu	Leu	Glu	Gln	Gly	Leu	Leu	
			1275					1280					1285			
tat	atg	cca	caa	gaa	ctt	act	gtg	tcc	gat	agc	gtg	ctg	gtt	ttt	gag	3941
Tyr	Met	Pro	Gln	Glu	Leu	Thr	Val	Ser	Asp	Ser	Val	Leu	Val	Phe	Glu	
	1290					1295					1300					
ctt	acg	gat	ata	gtc	cac	tgc	cgt	atg	gcc	gcc	cca	agc	cag	cga	aag	3989
Leu	Thr	Asp	Ile	Val	His	Cys	Arg	Met	Ala	Ala	Pro	Ser	Gln	Arg	Lys	
	1305					1310					1315					
gct	gtt	ctc	tca	acg	ctt	gtg	ggg	agg	tac	ggc	cgt	agg	act	aaa	tta	4037
Ala	Val	Leu	Ser	Thr	Leu	Val	Gly	Arg	Tyr	Gly	Arg	Arg	Thr	Lys	Leu	
1320					1325			1330								
tat	gag	gcg	gcg	cat	tca	gat	gtc	cgt	gag	tcc	cta	gcg	agg	ttt	atc	4085
Tyr	Glu	Ala	Ala	His	Ser	Asp	Val	Arg	Glu	Ser	Leu	Ala	Arg	Phe	Ile	
1335			1340					1345					1350			
ccc	acc	atc	ggg	cct	gtt	cgg	gct	acc	aca	tgt	gag	ctg	tac	gag	ctg	4133
Pro	Thr	Ile	Gly	Pro	Val	Arg	Ala	Thr	Thr	Cys	Glu	Leu	Tyr	Glu	Leu	
			1355				1360						1365			
gtt	gaa	gcc	atg	gta	gag	aag	ggc	cag	gac	gga	tct	gcc	gtc	cta	gag	4181
Val	Glu	Ala	Met	Val	Glu	Lys	Gly	Gln	Asp							

gat tgc aat aag ttt aca act ggt gag act atc gcc cat ggc aag gtt Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val 1400 1405 1410	4277
ggc cag ggc ata tcg gcc tgg agc aag acc ttc tgt gct ctg ttt ggc Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly 1415 1420 1425 1430	4325
ccg tgg ttc cgc gcc att gaa aag gaa ata ttg gcc cta ctc ccg cct Pro Trp Phe Arg Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro 1435 1440 1445	4373
aat atc ttt tat ggc gac gcc tat gag gag tca gtg ttt gct gcc gct Asn Ile Phe Tyr Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala 1450 1455 1460	4421
gtg tcc ggg gca ggg tca tgt atg gta ttt gaa aat gac ttc tca gag Val Ser Gly Ala Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu 1465 1470 1475	4469
ttt gac agt acc cag aat aat ttc tct ctc ggc ctt gag tgt gtg gtt Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val 1480 1485 1490	4517
atg gag gag tgc ggc atg ccc caa tgg tta att agg ttg tac cat ctg Met Glu Glu Cys Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu 1495 1500 1505 1510	4565
gtc cgg tca gcc tgg att ttg cag gcg ccg aag gag tct ctt aag ggg Val Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly 1515 1520 1525	4613
ttt tgg aag aag cac tct ggt gag cct ggt acc ctt ctc tgg aac act Phe Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr 1530 1535 1540	4661
gtc tgg aac atg gcg att ata gca cat tgc tay gag ttc cgt gac ttt Val Trp Asn Met Ala Ile Ile Ala His Cys Xaa Glu Phe Arg Asp Phe 1545 1550 1555	4709
cgt gtt gcc gcc ttc aag ggt gat gat tca gtg gtc ctc tgt agt gac Arg Val Ala Ala Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp 1560 1565 1570	4757
tac cga cag rgc cgt aac gcg gct gcc tta att gca ggc tgt ggg ctc Tyr Arg Gln Xaa Arg Asn Ala Ala Leu Ile Ala Gly Cys Gly Leu 1575 1580 1585 1590	4805
aaa ttg aag gtt gat tac cgc cct atc ggg cta tat gct gga gtg gtg Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val 1595 1600 1605	4853
gtg gcc ccc ggt ttg ggg aca ctg ccc gat gtg gtg cgt ttt gcc ggt Val Ala Pro Gly Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly 1610 1615 1620	4901
cgg tta tct gag aag aat tgg ggc cct ggc ccg gag cgt gct gag cag	4949

Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln	
1625	1630 1635
ctg cgt ctt gct gtt tgt gat ttc ctt cga ggg ttg acg aat gtt gcg	4997
Leu Arg Leu Ala Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala	
1640	1645 1650
cag gtc tgt gtt gat gtt gtg tcc cgt gtc tat gga gtt agc ccc ggg	5045
Gln Val Cys Val Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly	
1655	1660 1665 1670
ctg gta cat aac ctt att ggc atg ctg cag acc att gct gat ggc aag	5093
Leu Val His Asn Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys	
	1675 1680 1685
gcc cac ttt aca gar aat att aaa cct gtg ctt gac ctt aca aat tcc	5141
Ala His Phe Thr Xaa Asn Ile Lys Pro Val Leu Asp Leu Thr Asn Ser	
	1690 1695 1700
atc ata caa cgg gtg gaa tga ataacatgtc ttttgcacgc cccatgggat cacc	5196
Ile Ile Gln Arg Val Glu	
	1705
atg cgc cct agg gct gtt ctg ttg ttg ctc ttc gtg ctt ttg cct atg	5244
Met Arg Pro Arg Ala Val Leu Leu Leu Leu Phe Val Leu Leu Pro Met	
1710	1715 1720 1725
ctg ccc gcg cca ccg gcc ggc cag ccg tct ggc cgc cgt cgt ggg ccg	5292
Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg	
	1730 1735 1740
cgc agc ggc ggt gcc ggc ggt ggt ttc tgg ggt gac agg gtt gat tct	5340
Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser	
	1745 1750 1755
cag ccc ttc gcc ctc ccc tat att cat cca acc aac ccc ttc gcc gcc	5388
Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala	
	1760 1765 1770
gat gtc gtt tca caa ccc ggg gct gga act cgc cct cga cag ccg ccc	5436
Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro	
1775	1780 1785
cgc ccc ctt ggy tcc gct tgg cgt gac cag tcc cag cgc ccc tcc gct	5484
Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala	
1790	1795 1800 1805
gcc ccc cgt cgt cga tct gcc cca gct ggg gct gcg ccg ctg act gcc	5532
Ala Pro Arg Arg Arg Ser Ala Pro Ala Gly Ala Ala Pro Leu Thr Ala	
	1810 1815 1820
gtg tca ccg gct cct gac aca gcc cct gta cct gat gtt gac tca cgt	5580
Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg	
	1825 1830 1835
ggt gct att ctg cgc ccg cag tac aat ttg tcc acg tcc ccg ctc acg	5628
Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr	

1840	1845	1850	
tca tct gtc gct tcg ggt act aat ttg gtc ctc tat gct gcc ccg ctg Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu 1855 1860 1865			5676
aat ccc ctc ttg cct ctc cag gat ggt acc aac act cat att atg gct Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala 1870 1875 1880 1885			5724
act gag gca tcc aat tat gcc cag tat cgg gtt gtt cga gct aca atc Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile 1890 1895 1900			5772
cgt tat cgc ccg ctg gtg ccg aat gcc gtt ggt ggc tat gcc att tcc Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser 1905 1910 1915			5820
att tct ttc tgg ccc caa act aca act acc cct act tct gtc gat atg Ile Ser Phe Trp Pro Gln Thr Thr Thr Pro Thr Ser Val Asp Met 1920 1925 1930			5868
aat tct att act tcc acy gat gtt agg att ttg gtt cag ccc ggt att Asn Ser Ile Thr Ser Xaa Asp Val Arg Ile Leu Val Gln Pro Gly Ile 1935 1940 1945			5916
gcc tcc gag cta gtc atc ccc agt gag cgc ctt cat tac cgt aat caa Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln 1950 1955 1960 1965			5964
ggc tgg cgc tct gtt gag acc acg ggt gtg gct gag gag gag gct act Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr 1970 1975 1980			6012
tcc ggt ctg gta atg ctt tgc att cat ggc tct cct gtt aat tcc tac Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr 1985 1990 1995			6060
act aat aca cct tac act ggt gcg ctg ggg ctt ctt gat ttt gca cta Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu 2000 2005 2010			6108
gag ctt gaa ttt agg aat ttg aca ccc ggg aac acc aac acc cgt gtt Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val 2015 2020 2025			6156
tcc cgg tat acc agc aca gcc cgc cac cgg ctg cgc cgt ggt gct gat Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp 2030 2035 2040 2045			6204
ggg act gct gag ctt act acc aca gca gcc aca cgt ttc atg aag gac Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp 2050 2055 2060			6252
ctg cac ttc gct ggc acg aat ggc gtt ggt gag gtg ggt cgt ggt atc Leu His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile 2065 2070 2075			6300

6108
6156
6204
6252
6300

gcc ctg aca ctg ttc aat ctc gct gat acg ctt ctc ggc ggt tta ccg Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro 2080 2085 2090	6348
aca gaa ttg att tcg tcg gct ggg ggc caa ctg ttt tac tcc cgc ccg Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro 2095 2100 2105	6396
gtt gtc tca gcc aat ggc gag cca aca gta aag tta tat aca tct gtt Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val 2110 2115 2120 2125	6444
gag aat gcg cag caa gac aag ggc atc acc att cca cat gat ata gac Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp 2130 2135 2140	6492
ctg ggt gac tcc cgt gtg gtt atc cag gat tat gat aac cag cay gag Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln Xaa Glu 2145 2150 2155	6540
caa gac cga cct act ccg tca cct gcc ccc tct cgc ccc ttc tca gtt Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val 2160 2165 2170	6588
ctt cgt gcc aat gat gtt ttg tgg ctt tcc ctc act gcc gct gag tat Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr 2175 2180 2185	6636
gac cag act acg tat ggg tcg tcc acc aac cct atg tat gtc tct gac Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp 2190 2195 2200 2205	6684
aca gtt acg ctt gtt aat gtg gct act ggt gct cag gct gtt gcc cgc Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg 2210 2215 2220	6732
tcc ctt gat tgg tct aaa gtt act ctg gac ggc cgc ccc ctt act acc Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr 2225 2230 2235	6780
att cag cag tat tct aag aca ttt tat gtt ctc ccg ctc cgc ggg aag Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys 2240 2245 2250	6828
ctg tcc ttt tgg gag gct ggc acg act aag gcc ggc tac cct tac aat Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn 2255 2260 2265	6876
tat aat act acc gct agt gac caa att ttg att gag aat gcg gcc ggc Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly 2270 2275 2280 2285	6924
cac cgt gtc gct att tcc acc tat acc act agc tta ggt gcc ggt cct His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro 2290 2295 2300	6972

acc tcg atc tct gcg gtc ggc gta ctg gct cca cac tct gcc ctt gcc 7020
 Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala
 2305 2310 2315

gtt ctt gag gat act att gat tac ccc gcc cgt gcc cat act ttt gat 7068
 Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
 2320 2325 2330

gat ttt tgc ccg gag tgc cgt acc cta ggt ttg cag ggt tgt gca ttc 7116
 Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe
 2335 2340 2345

cag tct act att gct gag ctg cag cgt tta aaa atg aag gta ggt aaa 7164
 Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
 2350 2355 2360 2365

acc cgg gag tct taa ttaattcctt ctgtgcccc ttcgtagttt ctttcgcttt 7219
 Thr Arg Glu Ser
 2370

tattttcttat ttctgctttc cgcgctccct ggaaaaaaaa aaaaaaaaaa aaaaaaaaaa 7277

<210> 166

<211> 1708

<212> PRT

<213> Hepatitis E virus

<400> 166

Met Glu Ala His Gln Phe Ile Lys Ala Pro Gly Ile Thr Thr Ala Ile
 1 5 10 15

Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser Ala Leu Ala Asn Ala Val
 20 25 30

Val Val Arg Pro Phe Leu Ser Arg Val Gln Thr Glu Ile Leu Ile Asn
 35 40 45

Leu Met Gln Pro Arg Gln Leu Val Phe Arg Pro Glu Val Leu Trp Asn
 50 55 60

His Pro Ile Gln Arg Val Ile His Asn Glu Leu Glu Gln Tyr Cys Arg
 65 70 75 80

Ala Arg Ala Gly Arg Cys Leu Glu Val Gly Ala His Pro Arg Ser Ile
 85 90 95

Asn Asp Asn Pro Asn Val Leu His Arg Cys Phe Leu Arg Pro Val Gly
 100 105 110

Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro Thr Arg Gly Pro Ala Ala
 115 120 125

Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu Pro Pro Val Asp Arg Thr
 130 135 140

Tyr Cys Phe Asp Gly Phe Ser Arg Cys Ala Phe Ala Ala Glu Thr Gly

145		150		155		160									
Val	Ala	Leu	Tyr	Ser	Leu	His	Asp	Leu	Trp	Pro	Ala	Asp	Val	Ala	Glu
				165					170					175	
Ala	Met	Ala	Arg	His	Gly	Met	Thr	Arg	Leu	Tyr	Ala	Ala	Leu	His	Leu
			180					185					190		
Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly	Thr	Tyr	His	Thr	Thr	Ser	Tyr
		195					200					205			
Leu	Leu	Ile	His	Asp	Gly	Asn	Arg	Ala	Val	Val	Thr	Tyr	Glu	Gly	Asp
	210					215					220				
Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val	Ser	Ile	Leu	Arg	Ala	Trp	Ile
225					230					235					240
Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His	Pro	Leu	Val	Ile	Glu	Arg	Val
			245						250					255	
Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala	Pro	Glu
			260					265					270		
Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	Pro	Arg	Ser	Thr	Glu	Val	Tyr
		275					280					285			
Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	Ser	Pro	Ser	Leu	Phe	Pro	Ser
	290					295					300				
Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	Ala	Val	Pro	Val	His	Ile	Trp
305					310					315					320
Asp	Xaa	Leu	Met	Leu	Phe	Gly	Ala	Thr	Leu	Xaa	Asp	Gln	Ala	Phe	Cys
			325						330					335	
Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	Gly	Ile	Ser	Tyr	Lys	Val	Thr
			340					345					350		
Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly	Trp	Asn	Ala	Ser	Glu	Asp	Ala
		355					360					365			
Leu	Thr	Ala	Val	Ile	Thr	Ala	Ala	Tyr	Leu	Thr	Ile	Cys	His	Gln	Arg
	370					375					380				
Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	Gly	Met	Arg	Arg	Leu	Glu	Val
385					390					395					400
Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	Leu	Tyr	Ser	Trp	Leu	Phe	Glu
			405						410					415	
Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	Arg	Gln	Leu	Gln	Phe	Tyr	Ala
			420					425					430		
Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	Phe	His	Leu	Xaa	Pro	Arg	Xaa
		435					440					445			
Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys	Arg	Cys	Arg	Thr	Phe	Leu	Lys

450	455	460
Lys Val Ala Gly Lys Phe Cys Cys Phe Met Arg Trp Leu Gly Gln Glu 465 470 475 480		
Cys Thr Cys Phe Leu Glu Pro Ala Glu Gly Leu Val Gly Asp Gln Gly 485 490 495		
His Asp Asn Glu Ala Tyr Glu Gly Ser Glu Val Asp Pro Ala Glu Pro 500 505 510		
Ala His Leu Asp Val Ser Gly Thr Tyr Ala Val His Gly His Gln Leu 515 520 525		
Glu Ala Leu Tyr Arg Ala Leu Asn Val Pro His Asp Ile Ala Ala Arg 530 535 540		
Ala Ser Arg Leu Thr Ala Thr Val Glu Leu Val Ala Ser Pro Asp Arg 545 550 555 560		
Leu Glu Cys Arg Thr Val Leu Gly Asn Lys Thr Phe Arg Thr Thr Val 565 570 575		
Val Asp Gly Ala His Leu Glu Ala Asn Gly Pro Glu Glu Tyr Val Leu 580 585 590		
Ser Phe Asp Ala Ser Arg Gln Ser Met Gly Ala Gly Ser His Ser Leu 595 600 605		
Thr Tyr Glu Leu Thr Pro Ala Gly Leu Gln Val Lys Ile Ser Ser Asn 610 615 620		
Gly Leu Asp Cys Thr Ala Thr Phe Pro Xaa Gly Gly Ala Pro Ser Ala 625 630 635 640		
Ala Pro Gly Glu Val Xaa Ala Phe Cys Ser Ala Leu Tyr Arg Tyr Asn 645 650 655		
Arg Phe Thr Gln Arg His Ser Leu Thr Gly Gly Leu Trp Leu His Pro 660 665 670		
Glu Gly Leu Leu Gly Ile Phe Pro Pro Phe Ser Pro Gly His Ile Trp 675 680 685		
Glu Ser Ala Asn Pro Phe Cys Gly Glu Gly Thr Leu Tyr Thr Arg Thr 690 695 700		
Trp Ser Thr Ser Gly Phe Ser Ser Asp Phe Ser Pro Pro Glu Ala Ala 705 710 715 720		
Ala Pro Ala Ser Ala Ala Ala Pro Gly Leu Pro Tyr Pro Thr Pro Pro 725 730 735		
Val Ser Asp Ile Trp Val Leu Pro Pro Pro Ser Glu Glu Ser His Val 740 745 750		
Asp Ala Ala Ser Val Pro Ser Val Pro Glu Pro Ala Gly Leu Thr Ser		

755					760					765				
Pro	Ile	Val	Leu	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Val	Arg	Lys	Pro
770					775					780				
Ala	Thr	Ser	Pro	Pro	Pro	Arg	Thr	Arg	Arg	Leu	Leu	Tyr	Thr	Tyr
785					790					795				800
Asp	Gly	Ala	Lys	Val	Tyr	Ala	Gly	Ser	Leu	Xaa	Glu	Ser	Asp	Cys
				805					810					815
Trp	Leu	Val	Asn	Ala	Ser	Asn	Pro	Gly	His	Arg	Pro	Gly	Gly	Gly
			820					825					830	Leu
Cys	His	Ala	Phe	Tyr	Gln	Arg	Phe	Pro	Glu	Ala	Phe	Tyr	Ser	Thr
		835					840					845		Glu
Phe	Ile	Met	Arg	Glu	Gly	Leu	Ala	Ala	Tyr	Thr	Leu	Thr	Pro	Arg
		850				855					860			Pro
Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg	Val	Glu	Gln	Asn	Pro
865					870					875				Lys
Arg	Leu	Glu	Ala	Ala	Tyr	Arg	Glu	Thr	Cys	Ser	Arg	Arg	Gly	Thr
				885					890					895
Ala	Tyr	Pro	Leu	Leu	Gly	Ser	Gly	Ile	Tyr	Gln	Val	Pro	Val	Ser
			900					905					910	Leu
Ser	Phe	Asp	Ala	Trp	Glu	Arg	Asn	His	Arg	Pro	Gly	Asp	Glu	Leu
		915					920					925		Tyr
Leu	Thr	Glu	Pro	Ala	Ala	Ala	Trp	Phe	Glu	Ala	Asn	Lys	Pro	Ala
		930				935					940			Gln
Pro	Ala	Leu	Thr	Ile	Thr	Glu	Asp	Thr	Ala	Arg	Thr	Ala	Asn	Leu
945					950					955				960
Leu	Glu	Ile	Asp	Ala	Ala	Thr	Glu	Val	Gly	Arg	Ala	Cys	Ala	Gly
				965					970					975
Thr	Ile	Ser	Pro	Gly	Ile	Val	His	Tyr	Gln	Phe	Thr	Ala	Gly	Val
			980					985					990	Pro
Gly	Ser	Gly	Lys	Ser	Arg	Ser	Ile	Gln	Gln	Gly	Asp	Val	Asp	Val
		995					1000					1005		Val
Val	Val	Pro	Thr	Arg	Glu	Leu	Arg	Asn	Ser	Trp	Arg	Arg	Arg	Gly
		1010				1015					1020			Phe
Ala	Ala	Phe	Thr	Pro	His	Thr	Ala	Ala	Arg	Val	Thr	Ile	Gly	Arg
025					1030					1035				1040
Val	Val	Ile	Asp	Glu	Ala	Pro	Ser	Leu	Pro	Pro	His	Leu	Leu	Leu
				1045				1050					1055	
His	Met	Gln	Arg	Ala	Ser	Ser	Val	His	Leu	Leu	Gly	Asp	Pro	Asn
														Gln

1060	1065	1070
Ile Pro Ala Ile Asp Phe Glu His Ala Gly Leu Val Pro Ala Ile Arg 1075 1080 1085		
Pro Glu Leu Ala Pro Thr Ser Trp Trp His Val Thr His Arg Cys Pro 1090 1095 1100		
Ala Asp Val Cys Glu Leu Ile Arg Gly Ala Tyr Pro Lys Ile Gln Thr 105 1110 1115 1120		
Thr Ser Arg Val Leu Arg Ser Leu Phe Trp Asn Glu Pro Ala Ile Gly 1125 1130 1135		
Gln Lys Leu Val Phe Thr Gln Ala Ala Lys Ala Ala Asn Pro Gly Ala 1140 1145 1150		
Ile Thr Val His Glu Ala Gln Gly Ala Thr Phe Thr Glu Thr Thr Ile 1155 1160 1165		
Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile Gln Ser Ser Arg Ala His 1170 1175 1180		
Ala Ile Val Ala Leu Thr Arg His Thr Glu Lys Cys Val Ile Leu Asp 185 1190 1195 1200		
Ala Pro Gly Leu Leu Arg Glu Val Gly Ile Ser Asp Val Ile Val Asn 1205 1210 1215		
Asn Phe Phe Leu Ala Gly Gly Glu Val Gly His His Arg Pro Ser Val 1220 1225 1230		
Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu Gly Thr Leu Gln Ala Phe 1235 1240 1245		
Pro Pro Ser Cys Gln Ile Ser Ala Tyr His Gln Leu Ala Glu Glu Leu 1250 1255 1260		
Gly His Arg Pro Ala Pro Val Ala Ala Val Leu Pro Pro Cys Pro Glu 265 1270 1275 1280		
Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln Glu Leu Thr Val Ser Asp 1285 1290 1295		
Ser Val Leu Val Phe Glu Leu Thr Asp Ile Val His Cys Arg Met Ala 1300 1305 1310		
Ala Pro Ser Gln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr 1315 1320 1325		
Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala His Ser Asp Val Arg Glu 1330 1335 1340		
Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly Pro Val Arg Ala Thr Thr 345 1350 1355 1360		
Cys Glu Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp		

1365										1370										1375																			
Gly Ser Ala Val Leu Glu Leu Asp Leu Cys Asn Arg Asp Val Ser Arg																																							
1380										1385										1390																			
Ile Thr Phe Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr																																							
1395										1400										1405																			
Ile Ala His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr																																							
1410										1415										1420																			
Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Glu Ile																																							
425										1430										1435										1440									
Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr Gly Asp Ala Tyr Glu Glu																																							
										1445										1450										1455									
Ser Val Phe Ala Ala Ala Val Ser Gly Ala Gly Ser Cys Met Val Phe																																							
										1460										1465										1470									
Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu																																							
										1475										1480										1485									
Gly Leu Glu Cys Val Val Met Glu Glu Cys Gly Met Pro Gln Trp Leu																																							
										1490										1495										1500									
Ile Arg Leu Tyr His Leu Val Arg Ser Ala Trp Ile Leu Gln Ala Pro																																							
505										1510										1515										1520									
Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys His Ser Gly Glu Pro Gly																																							
										1525										1530										1535									
Thr Leu Leu Trp Asn Thr Val Trp Asn Met Ala Ile Ile Ala His Cys																																							
										1540										1545										1550									
Xaa Glu Phe Arg Asp Phe Arg Val Ala Ala Phe Lys Gly Asp Asp Ser																																							
										1555										1560										1565									
Val Val Leu Cys Ser Asp Tyr Arg Gln Xaa Arg Asn Ala Ala Ala Leu																																							
										1570										1575										1580									
Ile Ala Gly Cys Gly Leu Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly																																							
585										1590										1595										1600									
Leu Tyr Ala Gly Val Val Val Ala Pro Gly Leu Gly Thr Leu Pro Asp																																							
										1605										1610										1615									
Val Val Arg Phe Ala Gly Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly																																							
										1620										1625										1630									
Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala Val Cys Asp Phe Leu Arg																																							
										1635										1640										1645									
Gly Leu Thr Asn Val Ala Gln Val Cys Val Asp Val Val Ser Arg Val																																							
										1650										1655										1660									
Tyr Gly Val Ser Pro Gly Leu Val His Asn Leu Ile Gly Met Leu Gln																																							

665 1670 1675 1680
 Thr Ile Ala Asp Gly Lys Ala His Phe Thr Xaa Asn Ile Lys Pro Val
 1685 1690 1695

Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg Val Glu
 1700 1705

<210> 167
 <211> 660
 <212> PRT
 <213> Hepatitis E virus

<400> 167

Met Arg Pro Arg Ala Val Leu Leu Leu Leu Phe Val Leu Leu Pro Met
 1 5 10 15

Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg
 20 25 30

Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser
 35 40 45

Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala
 50 55 60

Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro
 65 70 75 80

Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala
 85 90 95

Ala Pro Arg Arg Arg Ser Ala Pro Ala Gly Ala Ala Pro Leu Thr Ala
 100 105 110

Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg
 115 120 125

Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr
 130 135 140

Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu
 145 150 155 160

Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala
 165 170 175

Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile
 180 185 190

Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser
 195 200 205

Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met
 210 215 220

Asn	Ser	Ile	Thr	Ser	Xaa	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	Ile	225	230	235	240
Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	Gln	245	250	255	
Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	Ala	Thr	260	265	270	
Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	Tyr	275	280	285	
Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	Leu	290	295	300	
Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	Val	305	310	315	320
Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	Asp	325	330	335	
Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp	340	345	350	
Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile	355	360	365	
Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro	370	375	380	
Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro	385	390	395	400
Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val	405	410	415	
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp	420	425	430	
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	Xaa	Glu	435	440	445	
Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val	450	455	460	
Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr	465	470	475	480
Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr	Val	Ser	Asp	485	490	495	
Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg	500	505	510	
Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Thr	Thr	515	520	525	

Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys
530 535 540

Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
545 550 555 560

Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly
565 570 575

His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
580 585 590

Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala
595 600 605

Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
610 615 620

Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe
625 630 635 640

Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
645 650 655

Thr Arg Glu Ser
660

<210> 168

<211> 122

<212> PRT

<213> Hepatitis E virus

<220>

<223> us2 orf3

<400> 168

Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
1 5 10 15

Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
20 25 30

His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala
35 40 45

Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
50 55 60

Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser Phe
65 70 75 80

His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Leu
85 90 95

Xaa Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro Pro Val
100 105 110

Val Asp Leu Pro Gln Leu Gly Leu Arg Arg
 115 120

<210> 169
 <211> 33
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> M 4-2

<400> 169
 Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser
 1 5 10 15

Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg
 20 25 30

Arg

<210> 170
 <211> 48
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> M 3-2e

<400> 170
 Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe Asp Asp Phe Cys Pro
 1 5 10 15

Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val
 20 25 30

Ala Glu Leu Gln Arg Leu Lys Val Lys Val Gly Lys Thr Arg Glu Leu
 35 40 45

<210> 171
 <211> 33
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> B 4-2

<400> 171
 Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro Ser
 1 5 10 15

Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly Pro Arg
 20 25 30

Arg

<210> 172
 <211> 48
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> B 3-2e

<400> 172
 Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
 1 5 10 15
 Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val
 20 25 30
 Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Leu
 35 40 45

<210> 173
 <211> 33
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> ORF3 (u4.2)

<400> 173
 Asp Ser Arg Pro Ala Pro Ser Val Pro Leu Gly Val Thr Ser Pro Ser
 1 5 10 15

Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
 20 25 30

Arg

<210> 174
 <211> 48
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> ORF2 (u3.2e)

<400> 174

Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
 1 5 10 15

Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile
 20 25 30

Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser
 35 40 45

<210> 175

<211> 33

<212> PRT

<213> Hepatitis E virus

<220>

<223> US 4-2

<400> 175

Asp Ser Arg Pro Ala Pro Ser Val Pro Leu Gly Val Thr Ser Pro Ser
 1 5 10 15

Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
 20 25 30

Cys

<210> 176

<211> 48

<212> PRT

<213> Hepatitis E virus

<220>

<223> US 3-2e

<400> 176

Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
 1 5 10 15

Glu Cys Arg Thr Leu Gly Val Gln Gly Cys Ala Phe Gln Ser Thr Ile
 20 25 30

Ala Glu Val Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Val
 35 40 45

<210> 177

<211> 21

<212> DNA
 <213> Hepatitis E virus

<220>
 <223> HEVConsORF1-s2

<400> 177
 ctgccytkgc gaatgctgtg g 21

<210> 178
 <211> 24
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> HEVConsORF1-a2

<400> 178
 ggcagwrtac carcgctgaa catc 24

<210> 179
 <211> 294
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> z12-orf1 (G.S.)

<400> 179
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 tgctgtggtg gttcggccgt ttttatctcg tttacagact gagattctta ttaatttgat 120
 gcaacccccga cagttggtct ttcgacctga ggtgttctgg aaccatccca tccaacgtgt 180
 tatacataat gaattggagc agtactgccg ggccccggcc ggtcgctgtc tggaaattgg 240
 agcccatcca aggtcaatca atgataatcc taatgttctg catcggtgtt tcct 294

<210> 180
 <211> 418
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> z12-orf1.con

<400> 180
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 tgcaacccccg acagttggtc tttcgacctg aggtgttctg gaaccatccc atccaacgtg 180

ttatacataa tgaattggag cagtactgcc gggcccgggc cggtcgctgt ctggaaattg 240
gagcccatcc aaggtcaatc aatgataatc ctaatgttct gcatcgggtgc tttttacgac 300
cggtcggggag ggacgttcag cgctggtact ccgccccac ccgtggcccc gcggccaact 360
gccgccggtc tgcgctgcgt ggtctcccc ctgtcgaccg cacttactgc ctcgatgg 418

<210> 181
<211> 197
<212> DNA
<213> Hepatitis E virus

<220>
<223> z12-orf2.con

<400> 181
gacagaatta atttcgtcgg ctgggggtca actgttctac tcccgcctg tcgtctcagc 60
caatggcgag ccgactgtca agttatacac atctgttgag aatgcacagc aggataaggg 120
gatagctatt ccacatgaca tagatttggg cgactctcgt ttggtaatcc aggattatga 180
taaccaacac gaacaag 197

<210> 182
<211> 25
<212> DNA
<213> Hepatitis E virus

<220>
<223> HEVConsORF2/3-s1

<400> 182
gtatcggkyk gaatgaataa catgt 25

<210> 183
<211> 25
<212> DNA
<213> Hepatitis E virus

<220>
<223> HEVConsORF2/3-a1

<400> 183
aggggttggt tggatgaata taggg 25

<210> 184
<211> 234
<212> DNA
<213> Hepatitis E virus

<220>

<223> z12-orf23.con

<400> 184

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gggttgttct gttgttgttc ctctgttttc tgcctatgct gcccgcgcca ccggccggcc 120
agycgactgg ccgcctcgtt gggcgggcgca gcggcggtgc cggcggtggt ttctgggggtg 180
acagggttga ttctcagccc ttccgctctc cctatatcca tccaaccaac ccct 234

<210> 185

<211> 890

<212> DNA

<213> Hepatitis E virus

<220>

<223> z12-3p.race

<400> 185

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caggattacg ataatcagca cgagcaggac cggcccaccc ctctgcccgc cccgtctcgt 180
cctttctcgg tcctccgcgc taatgatgct ttgtggcttt ctctaccgc tgctgagtat 240
gaccagacta catatgggtc gtccaccaac ccgatgtatg tctcagacac tgttacattt 300
gtcaatgtgg ccacaggggc tcaggctgtc gcccgttctc ttgattgggc taaagttacc 360
ctggacggcc gccctcttac taccatccag cagtactcta agacatttta tgttctocca 420
cttcgcggga agttatcttt ttgggaggct ggcacaacta aagccggtta cccttataat 480
tataacacaa ctgctagtga ccagattctg attgaaaacg cggctggcca tcgtgtcgtc 540
atatctactt atactactag cctgggcgcc ggccctgtgt cagtttctgc ggttggtgtg 600
ttagcccccac actcgagcct tgctattctt gaagacactg ttgactatcc ggcccggtgc 660
cacacttttg atgacttctg tccggaatgc cgtgccctgg gtctgcaggg gtgtgctttt 720
caatctacta tcgctgagct ccagcgtctt aaaatgaagg taggcaaaac ccgggagttt 780
taattaattc ttcttgtgcc cccttcacgg ttctcgcttt atttctttct tctgcctccc 840
gcgctccctg gaaaaaaaaa aaaaaaaaaa gtactagtcg acgcgtggcc 890

<210> 186

<211> 919

<212> DNA

<213> Hepatitis E virus

<220>

<223> z12-3p.con

<400> 186

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 caatggcgag ccgactgtca agttatacac atctgttgag aatgcacagc aggataaggg 120
 gatagctatt ccacatgaca tagatttggg cgactctcgt ttggtaatcc aggattacga 180
 taatcagcac gagcaggacc ggcccacccc ttgcgccgcc ccgtctcgtc ctttctcggg 240
 cctccgcgct aatgatgctt tgtggctttc tcttaccgct gctgagtatg accagactac 300
 atatgggtcg tccaccaacc cgatgtatgt ctcagacact gttacatttg tcaatgtggc 360
 cacaggggct caggctgtcg cccgttctct tgatttgtct aaagttaccg tggacggccg 420
 ccctcttact accatccagc agtactctaa gacattttat gttctccac ttgcgggaa 480
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 aaaaaaaaaa aaaaaaaaaa 919

<210> 187

<211> 138

<212> PRT

<213> Hepatitis E virus

<220>

<223> z12-orfl.pep

<400> 187

Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Gly Ala Ala Asn Ser
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 Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Leu Gln
 20 25 30
 Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
 35 40 45
 Pro Glu Val Phe Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
 50 55 60

Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Ile Gly
 65 70 75 80
 Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
 85 90 95
 Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
 100 105 110
 Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
 115 120 125
 Pro Pro Val Asp Arg Thr Tyr Cys Leu Asp
 130 135

<210> 188
 <211> 61
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> z12-orf2-5'.pep

<400> 188
 Met Arg Pro Arg Val Val Leu Leu Leu Phe Leu Val Phe Leu Pro Met
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 Leu Pro Ala Pro Pro Ala Gly Gln Xaa Thr Gly Arg Arg Arg Gly Arg
 20 25 30
 Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser
 35 40 45
 Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro
 50 55 60

<210> 189
 <211> 276
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> z12-orf2-3'.pep

<400> 189
 Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

Leu Gly Asp Ser Arg Leu Val Ile Gln Asp Tyr Asp Asn Gln His Glu
50 55 60

Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val
65 70 75 80

Leu Arg Ala Asn Asp Ala Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr
85 90 95

Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp
100 105 110

Thr Val Thr Phe Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg
115 120 125

Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr
130 135 140

Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys
145 150 155 160

Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
165 170 175

Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly
180 185 190

His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
195 200 205

Val Ser Val Ser Ala Val Gly Val Leu Ala Pro His Ser Ser Leu Ala
210 215 220

Ile Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
225 230 235 240

Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe
245 250 255

Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
260 265 270

Thr Arg Glu Phe
275

<210> 190

<211> 74

<212> PRT

<213> Hepatitis E virus

<220>

<223> z12-orf3.pep

<400> 190

Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
1 5 10 15

Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
 20 25 30
 His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala
 35 40 45
 Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
 50 55 60
 Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro
 65 70

<210> 191
 <211> 408
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> pJOorf3-29.seq

<400> 191
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 ctggccgccc tcgtgggcgg cgcagcggcg gtgcccggcg tggtttctgg ggtgacaggg 180
 ttgattctca gcccttcgcc ctccctata ttcattcaac caacccttc gccgccgatg 240
 tcgtttcaca acccgggggt ggaactcgcc ctgcacagcc gcccgcgcc cttgggtccg 300
 cttggcgtga ccagtccag cgccttcctg ctgccccccg tcgtcgatct gcccagctt 360
 ggtctgcgcc gcgactacaa ggacgacgat gacaagtaat aaggatcc 408

<210> 192
 <211> 1026
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> cksorf2m-2.seq

<400> 192
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 aaggacctgc acttcgctgg cacgaatggc gttggtgagg tgggtcgtgg tatcgccctg 120
 aactgttca atctcgctga tacgcttctc ggcggtttac cgacagaatt gatttcgctg 180
 gctggggggc aactgtttta ctcccgcccg gttgtctcag ccaatggcga gccaacagta 240
 aagttatata catctgttga gaatgcgcag caagacaagg gcatcaccat tccacatgat 300

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aaaatgaagg taggtaaaac ccgggagttc gactacaagg acgacgatga caagtaataa 1020
ggatcc 1026

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<210> 193
<211> 1389
<212> DNA
<213> Hepatitis E virus

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<220>
<223> CKSORF32M-3.seq

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ctggccgccc tcgtgggccc cgtagcggcg gtgcccggcg tggtttctgg ggtgacaggg 180
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ctgacactgt tcaatctcgc tgatacgtt ctggcggtt taccgacaga attgatttcg 540
tcggctgggg gccaaactgt ttactcccgc ccggttgtct cagccaatgg cgagccaaca 600
gtaaagttat atacatctgt tgagaatgcg cagcaagaca agggcatcac cattccacat 660

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gatatagacc tgggtgactc ccgtgtggtt atccaggatt atgataacca gcatgagcaa 720
gaccgaccta ctccgtcacc tgccccctct cgtcccttct cagttcttcg tgccaatgat 780
gttttgtggc tttccctcac tgccgctgag tatgaccaga ctacgtatgg gtcgtccacc 840
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gttgcccgtc cccttgattg gtctaaagtt actctggacg gccgccccct tactaccatt 960
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<210> 194

<211> 408

<212> DNA

<213> Hepatitis E virus

<220>

<223> plorf3-12.con

<400> 194

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<210> 195

<211> 1026

<212> DNA

<213> Hepatitis E virus

<220>

<223> plorf2.2-6.seq

<400> 195

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aactgtttca atctcgctga tacgcttctc ggcggtttac cgacagaatt gatttcgctg 180
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cctatgtatg tctctgacac agttacgctt gttaatgtgg ctactgggtc tcaggctgtt 540
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1026

<210> 196

<211> 1389

<212> DNA

<213> Hepatitis E virus

<220>

<223> PLORF32M-14-5.seq

<400> 196

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ctggccgccc tcgtgggcgg cgtagcggcg gtgcggcggg tggtttctgg ggtgacaggg 180
ttgattctca gcccttcgcc ctccctata ttcatccaac caacccttc gccgccgatg 240

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tcgtttcaca acccggggct ggaactcgcc ctgcacagcc gccccgcccc cttgggtccg 300
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 ggtctgcgcc gcggtgctga tgggactgct gagcttacta ccacagcagc cacacgtttc 420
 atgaaggacc tgcacttcgc tggcacgaat ggcgttggtg aggtgggtcg tggtatcgcc 480
 ctgacactgt tcaatctcgc tgatacgctt ctcggcggtt taccgacaga attgatttcg 540
 tcggctgggg gccaaactgtt ttactccgcg ccggttggtc cagccaatgg cgagccaaca 600
 gtaaagtatt atacatctgt tgagaatgcg cagcaagaca agggcâtcac cattccacat 660
 gatatagacc tgggtgactc ccgtgtgggt atccaggatt atgataacca gcatgagcaa 720
 gaccgaccta ctccgtcacc tgccccctct cgcaccttct cagttcttcg tgccaatgat 780
 gttttgtggc ttccctcac tgccgctgag tatgaccaga ctacgtatgg gtcgtccacc 840
 aacctatgt atgtctctga cacagttaag cttgttaatg tggctactgg tgctcaggct 900
 gttgcccgct cccttgattg gtctaaagtt actctggacg gccgccccct tactaccatt 960
 cagcagtatt ctaagacatt ttatgttctc ccgtccgcg ggaagctgtc cttttgggag 1020
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 tgccgtaccc taggtttgca gggttgtgca ttccagtcta ctattgctga gctccagcgt 1320
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<210> 197

<211> 74

<212> PRT

<213> Hepatitis E virus

<220>

<223> z12-orf3-5'.pep

<400> 197

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Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys	Pro	Arg
			20					25					30		

Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro
115 120 125

Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser
 130 135 140
 Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn
 145 150 155 160
 Pro Met Tyr Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly
 165 170 175
 Ala Gln Ala Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp
 180 185 190
 Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val
 195 200 205
 Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys
 210 215 220
 Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu
 225 230 235 240
 Ile Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr
 245 250 255
 Ser Leu Gly Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala
 260 265 270
 Pro His Ser Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala
 275 280 285
 Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly
 290 295 300
 Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu
 305 310 315 320
 Lys Met Lys Val Gly Lys Thr Arg Glu Ser Asp Tyr Lys Asp Asp Asp
 325 330 335
 Asp Lys

<210> 200
 <211> 338
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> plorf2.2-6.pep

<400> 200
 Glu Phe Met Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala
 1 5 10 15
 Thr Arg Phe Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly
 20 25 30

Glu Val Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr
 35 40 45
 Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln
 50 55 60
 Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val
 65 70 75 80
 Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr
 85 90 95
 Ile Pro His Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp
 100 105 110
 Tyr Asp Asn Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro
 115 120 125
 Ser Arg Pro Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser
 130 135 140
 Leu Thr Ala Ala Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn
 145 150 155 160
 Pro Met Tyr Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly
 165 170 175
 Ala Gln Ala Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp
 180 185 190
 Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val
 195 200 205
 Leu Pro Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys
 210 215 220
 Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu
 225 230 235 240
 Ile Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr
 245 250 255
 Ser Leu Gly Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala
 260 265 270
 Pro His Ser Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala
 275 280 285
 Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly
 290 295 300
 Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu
 305 310 315 320
 Lys Met Lys Val Gly Lys Thr Arg Glu Ser Asp Tyr Lys Asp Asp Asp
 325 330 335

Asp Lys

<210> 201
 <211> 37
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> Description of Artificial Sequence: Primer orf35p

<400> 201
 tatatgaatt catgaataac atgtcttttg catcgcc 37

<210> 202
 <211> 68
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> Description of Artificial Sequence: Primer orf33p

<400> 202
 tatatggatc cttattactt gtcacgctcg tcctttagt cgcggcgcag accaagctgg 60
 ggcagatc 68

<210> 203
 <211> 132
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> pJOorf3-29.pep

<400> 203
 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
 1 5 10 15
 Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys
 20 25 30
 Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala
 35 40 45
 Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser
 50 55 60
 Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met
 65 70 75 80
 Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala
 85 90 95

Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro
 100 105 110

Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp
 115 120 125

Asp Asp Asp Lys
 130

<210> 204

<211> 132

<212> PRT

<213> Hepatitis E virus

<220>

<223> plorf3-12.pep

<400> 204

Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
 1 5 10 15

Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys
 20 25 30

Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala
 35 40 45

Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser
 50 55 60

Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met
 65 70 75 80

Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala
 85 90 95

Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro
 100 105 110

Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp
 115 120 125

Asp Asp Asp Lys
 130

<210> 205

<211> 48

<212> DNA

<213> Hepatitis E virus

<220>

<223> Description of Artificial Sequence: Primer orf23

<400> 205

ctcagcagtc ccatacagcac cgcggcgcag accaagctgg ggcagatc

48

<210> 206

<211> 459

<212> PRT

<213> Hepatitis E virus

<220>

<223> CKSORF32M-3.pep

<400> 206

Glu	Phe	Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys
1				5					10					15	

Ala	Leu	Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys
			20					25					30		

Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Val
		35					40					45			

Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
	50					55					60				

Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75					80

Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
			85						90					95	

Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		

Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg	Gly	Ala	Asp	Gly
	115					120						125			

Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp	Leu
130						135					140				

His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile	Ala
145					150				155					160	

Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro	Thr
			165						170					175	

Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro	Val
		180						185					190		

Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val	Glu
	195						200					205			

Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp	Leu
210						215					220				

Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	Glu	Gln
225					230					235				240	

Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu
 245 250 255
 Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp
 260 265 270
 Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr
 275 280 285
 Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser
 290 295 300
 Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile
 305 310 315 320
 Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu
 325 330 335
 Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr
 340 345 350
 Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His
 355 360 365
 Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr
 370 375 380
 Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val
 385 390 395 400
 Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp
 405 410 415
 Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln
 420 425 430
 Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr
 435 440 445
 Arg Glu Ser Asp Tyr Lys Asp Asp Asp Asp Lys
 450 455

<210> 207

<211> 459

<212> PRT

<213> Hepatitis E virus

<220>

<223> PLORF32M-14-5.pep

<400> 207

Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
 1 5 10 15

Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys
 20 25 30

Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Val
 35 40 45
 Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser
 50 55 60
 Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met
 65 70 75 80
 Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala
 85 90 95
 Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro
 100 105 110
 Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Gly Ala Asp Gly
 115 120 125
 Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu
 130 135 140
 His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala
 145 150 155 160
 Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr
 165 170 175
 Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val
 180 185 190
 Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu
 195 200 205
 Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu
 210 215 220
 Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln
 225 230 235 240
 Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu
 245 250 255
 Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp
 260 265 270
 Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr
 275 280 285
 Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser
 290 295 300
 Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile
 305 310 315 320
 Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu
 325 330 335

Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr
340 345 350

Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His
355 360 365

Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr
370 375 380

Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val
385 390 395 400

Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp
405 410 415

Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln
420 425 430

Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr
435 440 445

Arg Glu Ser Asp Tyr Lys Asp Asp Asp Asp Lys
450 455

<210> 208

<211> 36

<212> DNA

<213> Hepatitis E virus

<220>

<223> Description of Artificial Sequence: Primer
orf2mid5p

<400> 208

tatatgaatt catgggtgct gatgggactg ctgagc

36

<210> 209

<211> 418

<212> DNA

<213> Hepatitis E virus

<220>

<223> 1440o1.seq

<220>

<221> CDS

<222> (3)..(416)

<400> 209

ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gcc aat 47
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
1 5 10 15

tcc gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtt 95

Ser	Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	
				20					25						30	
caa	act	gat	atc	ctt	att	aac	ctg	atg	caa	ccc	cgt	cag	ctt	gtg	ttc	143
Gln	Thr	Asp	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	
			35					40					45			
cgg	cct	gaa	gtt	ctc	tgg	aac	cat	ccg	atc	cag	cga	gtt	ata	cat	aat	191
Arg	Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	
			50				55					60				
gag	ctg	gaa	caa	tac	tgt	cga	gcc	cgc	gct	ggc	cgc	tgt	ctt	gag	gtg	239
Glu	Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	
			65				70				75					
ggc	gct	cac	cca	agg	tct	att	aat	gat	aac	ccc	aat	gtt	ctg	cac	cgg	287
Gly	Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	
	80					85				90					95	
tgc	ttt	ctc	cgc	ccg	gtt	ggg	aga	gac	gtc	cag	cgc	tgg	tat	tcc	gcc	335
Cys	Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	
				100					105					110		
ccc	act	cgt	ggc	cca	gcg	gct	aac	tgc	cgc	cgt	tct	gcg	cta	cgc	ggt	383
Pro	Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	
			115					120					125			
ttg	ccc	cct	gtc	gac	cgc	act	tac	tgt	yty	gat	gg					418
Leu	Pro	Pro	Val	Asp	Arg	Thr	Tyr	Cys	Xaa	Asp						
			130				135									
<210> 210																
<211> 138																
<212> PRT																
<213> Hepatitis E virus																
<400> 210																
Gly	Xaa	Thr	Thr	Xaa	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser	
	1			5					10					15		
Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	Gln	
			20					25					30			
Thr	Asp	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg	
			35				40					45				
Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	
			50			55					60					
Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	Gly	
			65			70			75						80	
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	Cys	
				85					90					95		
Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro	

100

105

110

Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
 115 120 125

Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
 130 135

<210> 211

<211> 197

<212> DNA

<213> Hepatitis E virus

<220>

<223> 1440o2.seq

<220>

<221> CDS

<222> (2)..(196)

<400> 211

g aca gaa ttr att tcg tcg gct gga ggt caa ctg ttc tac tcc cgc ccg 49
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15

ggt gtc tca gcc aat ggc gag ccg act gtt aag tta tac acc tct gtc 97
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30

gag aat gca cag cag gat aag ggc att gct ata cca cat gat ata gac 145
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

tta ggg gat tcc cgt gtg gtt ata caa gat tat gay aac car cay gaa 193
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

caa g 197
 Gln
 65

<210> 212

<211> 65

<212> PRT

<213> Hepatitis E virus

<400> 212

Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15

Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

Gln
 65

<210> 213
 <211> 418
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 2015-1.seq

<220>
 <221> CDS
 <222> (3)..(416)

<400> 213
 ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gct aac 47
 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
 1 5 10 15
 tct gcc ttg gcg aat gct gtg gtg gtc cgg ccg ttc ctg tcc cgc act 95
 Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr
 20 25 30
 cag act gat att ctt att aat ttg atg caa ccc cgg caa ctt gta ttc 143
 Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
 35 40 45
 cgc cct gag gtt ttg tgg aac cat ccg atc cag cga gtc ata cat aat 191
 Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
 50 55 60
 gag ctg gag cag tat tgc cgt gct cgt gct ggt cgc tgc ctg gag gtt 239
 Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
 65 70 75
 ggg gct cat cca aga tct atc aat gac aac cct aat gtt ctg cac cgg 287
 Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
 80 85 90 95
 tgt ttc ctc cgt ccg gtt ggg cga gac gta cag cgt tgg tat tct gcc 335
 Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
 100 105 110
 cct act cgc ggc ccg gcg gct aat tgc cgc cgt tcc gcg tta cgt ggc 383
 Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
 115 120 125
 cta cct cct gtc gac cgc act tac tgt yty gat gg 418
 Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
 130 135

<210> 214
 <211> 138
 <212> PRT
 <213> Hepatitis E virus

<400> 214

Gly	Xaa	Thr	Thr	Xaa	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser
1				5					10					15	
Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Thr	Gln
			20					25					30		
Thr	Asp	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg
	35						40					45			
Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu
	50					55					60				
Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	Gly
	65				70					75					80
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	Cys
				85					90					95	
Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro
			100					105					110		
Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu
		115					120					125			
Pro	Pro	Val	Asp	Arg	Thr	Tyr	Cys	Xaa	Asp						
	130						135								

<210> 215
 <211> 197
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 2015o2.seq

<220>
 <221> CDS
 <222> (2)..(196)

<400> 215

g	aca	gaa	ttr	att	tcg	tcg	gct	gga	ggc	cag	ctc	ttc	tac	tcc	cgc	cca	49
Thr	Glu	Xaa	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro		
	1					5				10				15			
gtc	gtc	tca	gcc	aat	ggc	gag	ccg	act	ggt	aaa	ttg	tat	aca	tcc	gtc		97
Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val		
			20					25					30				
gag	aat	gcg	cag	cag	gac	aag	ggc	att	gcc	ata	cca	cat	gat	ata	gat		145

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

cta gga gat tcc cgc gtg gtt atc cag gat tat gay aac car cay gaa 193
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

caa g 197
 Gln
 65

<210> 216
 <211> 65
 <212> PRT
 <213> Hepatitis E virus

<400> 216
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15

Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

Gln
 65

<210> 217
 <211> 251
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 14404-2.seq

<220>
 <221> CDS
 <222> (3)..(251)
 <223> orf2

<220>
 <223> orf3 from position 1 to position 165

<400> 217
 at att cat cca acc aac ccc ttt gcc tcc gac gtc gta tcg caa tcc 47
 Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser
 1 5 10 15

ggg gct gga gct cgc cct cga cag ccg gcc cgc ccc ctc ggc tcc tct 95
 Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser

	20	25	30	
tgg cgt gac cag tcc cag cgc ccc ccc gct gtc ccc cgt cgt cga tct				143
Trp Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Arg Ser				
	35	40	45	
acc cca act ggg gct gcg ccg cta act gct gtt tca cca gcg cct gat				191
Thr Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp				
	50	55	60	
acg gcc cca gtc cct gat gtt gac tct cgt ggc gct atc ttg cgc cgg				239
Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg				
	65	70	75	
cag tat aac cta				251
Gln Tyr Asn Leu				
80				

<210> 218
 <211> 83
 <212> PRT
 <213> Hepatitis E virus

<400> 218
 Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser Gly
 1 5 10 15
 Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser Trp
 20 25 30
 Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Arg Ser Thr
 35 40 45
 Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr
 50 55 60
 Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
 65 70 75 80
 Tyr Asn Leu

<210> 219
 <211> 55
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> 14404-2.seq orf3

<400> 219
 Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr Arg Asn Pro
 1 5 10 15
 Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu

20

25

30

Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Ser Pro Val Val Asp Leu
 35 40 45

Pro Gln Leu Gly Leu Arg Arg
 50 55

<210> 220

<211> 251

<212> DNA

<213> Hepatitis E virus

<220>

<223> 20154-2.seq

<220>

<221> CDS

<222> (3)..(251)

<223> orf2

<220>

<223> orf3 from position 1 to position 165

<400> 220

at att cat cca acc aac ccc ttt gcc gcc gac gtc gta tca caa ccc 47

Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro

1

5

10

15

ggg gct gga gct cgc cct cga cag ccg ccc cgc ccc ctc ggc tcc tct 95

Gly Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser

20

25

30

tgg cgt gat cag tcc cag cgc ccc tcc gct gcc ccc cgt cgt cga tct 143

Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser

35

40

45

acc cca gct ggg gct gcg ccg tta act gct gtt tcc cct gcg ccc gat 191

Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp

50

55

60

acg gcc cca gtc ccc gac gtt gat tcc cgt ggt gcc atc ctg cgc cgg 239

Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg

65

70

75

cag tat aac cta

251

Gln Tyr Asn Leu

80

<210> 221

<211> 83

<212> PRT

<213> Hepatitis E virus

<400> 221

Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro Gly
 1 5 10 15
 Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser Trp
 20 25 30
 Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser Thr
 35 40 45
 Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr
 50 55 60
 Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
 65 70 75 80
 Tyr Asn Leu

<210> 222
 <211> 55
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> 20154-2.seq orf3

<400> 222
 Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr His Asn Pro
 1 5 10 15
 Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu
 20 25 30
 Gly Val Ile Ser Pro Ser Ala Pro Pro Leu Pro Pro Val Val Asp Leu
 35 40 45
 Pro Gln Leu Gly Leu Arg Arg
 50 55

<210> 223
 <211> 48
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> US-2 3-2e

<400> 223
 Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
 1 5 10 15
 Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile
 20 25 30
 Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser

35

40

45

<210> 224
 <211> 33
 <212> PRT
 <213> Hepatitis E virus

<220>
 <223> US-2 4-2

<400> 224
 Asp Ser Arg Pro Ala Pro Leu Val Pro Leu Gly Val Thr Ser Pro Ser
 1 5 10 15

Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
 20 25 30

Arg

<210> 225
 <211> 450
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 5p.pile {hpesvp}

<400> 225
 ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgccct 60
 ggcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tcctcattaa 120
 cctaatagcaa cctcgccagc ttgttttccg ccccgagggt ttctggaatc atcccatcca 180
 gcgtgtcatc cataacgagc tggagcttta ctgccgcgcc cgctccggcc gctgtcttga 240
 aattggcgcc catccccgct caataaatga taatcctaata gtggtccacc gctgcttct 300
 ccgccctgtt gggcgtgatg ttcagcgctg gtatactgct ccactcgcg ggcgggctgc 360
 taattgccgg cgttcgcgcg tgcgcgggct tcccgctgct gaccgcactt actgcctcga 420
 cgggttttct ggctgtaact ttcccgccga 450

<210> 226
 <211> 450
 <212> DNA
 <213> Hepatitis E virus

<220>

<223> 5p.pile {hpeuigh}

<400> 226

```
ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca attctgccct 60
tgcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tccttattaa 120
cctaatagcaa cctcgccagc ttgttttccg ccccgagggtt ttctggaacc accccatcca 180
gcgtgtcatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgccttga 240
aattggtgcc caccctcgct caataaacga caatccta atgtgtccacc gctgcttcc 300
ccgccctgcc gggcgtgatg ttcagcggtg gtatactgct cctaccgcgc ggcgggctgc 360
taattgccgg ggttccgcac tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420
cgggttttct ggctgtaact ttccgcgcga 450
```

<210> 227

<211> 450

<212> DNA

<213> Hepatitis E virus

<220>

<223> 5p.pile {hpea}

<400> 227

```
ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgccct 60
tgcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tccttattaa 120
cctaatagcaa cctcgccagc ttgttttccg ccccgagggtt ttctggaacc atcccatcca 180
gcgtgttatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgcctoga 240
aattggtgcc caccctcgct caataaatga caatccta atgtgtccacc gttgcttcc 300
ccgtcctgcc gggcgtgatg ttcagcggtg gtatactgcc cctaccgcgc ggcgggctgc 360
taattgccgg cgttccgcgc tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420
cgggttttct ggctgtaact ttccgcgcga 450
```

<210> 228

<211> 446

<212> DNA

<213> Hepatitis E virus

<220>

<223> 5p.pile {840455p}

<400> 228

```
cctggcatta ctactgcat tgagcaggct gctctggctg cggccaattc tgccttggcg 60
```

```

aatgctgtgg tggttcggcc gtttttatct cgcgtgcaaa ccgagattct tattaatttg 120
atgcaacccc ggcagttggt tttccgccct gaggtacttt ggaatcaccc tatccagcgg 180
gttatacata atgaattaga acagtactgc cgggctcggg ctggtcggtg cttggagggt 240
ggagctcacc caagatccat taatgacaac cccaacgttc tgcacggtg tttccttaga 300
ccggttggcc gagatgttca gcgctggtac tctgccccca cccgcggccc tgcgggtaat 360
tgccgccgct ccgcgttgcg tgggtctccc cccgctgacc gcacttactg ctttgatgga 420
ttctcccgtt gtgcttttgc tgcaga 446

```

```

<210> 229
<211> 450
<212> DNA
<213> Hepatitis E virus

```

```

<220>
<223> 5p.pile {hpenssp}

```

```

<400> 229
ggctcctggc atcactactg ctattgagca agcagctcta gcagcggcca actccgccct 60
tgcgaatgct gtggtggtcc ggcctttcct ttcccatcag caggttgaga tccttataaa 120
tctcatgcaa cctcggcagc tgggtgttctg tcctgagggt ttttggaatc acccgattca 180
acgtgttata cataatgagc ttgagcagta ttgccgtgct cgctcggggtc gctgccttga 240
gattggagcc caccacgct ccattaatga taatcctaata gtccctccatc gctgctttct 300
ccaccccgtc ggccgggatg ttcagcgtg gtacacagcc ccgactaggg gacctgcggc 360
gaactgtcgc cgctcggcac ttcgtggtct gccaccagcc gaccgcactt actgttttga 420
tggttttgcc ggctgccgtt ttgcgcgca 450

```

```

<210> 230
<211> 450
<212> DNA
<213> Hepatitis E virus

```

```

<220>
<223> 5p Consensus

```

```

<220>
<221> variation
<222> ()..(450)
<223> The nucleotide identity of each n is indicated in
      Figure 9.

```

```

<400> 230
nnnnccctggc atnactactg cnattgagca ngcnctctn gncgcggcca antcngcct 60

```

ngcgaatgct gtggtngttn ggcenntnt ntncnnnnng cannnngaga tncnatnaa 120
 nntnatgcaa ccncgncagn tngtnttncg nccngaggtn ntntggaanc anccnatnca 180
 ncgngtnatn cataangann tngancnnta ntgncngcn cgnncnggnc gntgnntnga 240
 nnttgngcn canccnngnt cnatnaanga naancnaa gtnntncanc gntgnttnc 300
 nnnncngnn ggncgngatg ttcagcngtg gtanncngcn ccnacnngng gncncngnc 360
 naantgncgn ngntcngcn tncngngnct nccnnngcn gaccgcactt actgnntnga 420
 nggnttnncn ngntgnnnnt ttnncngca 450

<210> 231

<211> 300

<212> DNA

<213> Hepatitis E virus

<220>

<223> 3p.pile {hpea} shown in Figure 9B

<400> 231

actgagtcag tgaagccagt gcttgacctg acaaattcaa ttctgtgtcg ggtggaatga 60
 ataacatgtc ttttgctgcg cccatgggtt cgcgaccatg cgcctcggc ctattttgc 120
 gttgtcctc atgtttctgc ctatgtgcc cgcgccaccg cccggtcagc cgtctggccg 180
 ccgtcgtggg cggcgcagcg gcggttcggg cggtggtttc tggggtgacc gggttgattc 240
 tcagcccttc gcaatccct atattcatcc aaccaacccc ttgcctcccg atgtcaccgc 300

<210> 232

<211> 300

<212> DNA

<213> Hepatitis E virus

<220>

<223> 3p.pile {hpeuigh} shown in Figure 9B

<400> 232

actgagtcgg tgaagccagt gctcgacttg acaaattcaa tcctgtgtcg ggtggaatga 60
 ataacatgtc ttttgctgcg cccatgggtt ggcgaccatg cgcctcggc ctattttgc 120
 gttgtcctc atgtttctgc ctatgtgcc cgcgccaccg cccggtcagc cgtctggccg 180
 ccgtcgtggg cggcgcagcg gcggttcggg cggtggtttc tggggtgacc gggttgattc 240
 tcagcccttc gcaatccct atattcatcc aaccaacccc ttgcctcccg atgtcaccgc 300

<210> 233

<211> 300
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {hpesvp} shown in Figure 9B

<400> 233
 actgagtcag taaaaccagt gctcgacttg acaaattcaa tcttggtgctg ggtggaatga 60
 ataacatgtc ttttgctgcg cccatggggt cgcgaccatg cgccctcggc ctattttggt 120
 gctgctcctc atgtttttgc ctatgctgcc cgcgccaccg cccggtcagc cgtctggccg 180
 ccgtcgtggg cggcgcagcg gcggttccgg cggtggtttc tggggtgacc gggttgattc 240
 tcagcccttc gcaatccctt atattcatcc aaccaacccc ttcgcccccg atgtcaccgc 300

<210> 234
 <211> 300
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {hpenssp} shown in Figure 9B

<400> 234
 acagagtctg ttaagcctat acttgacett acacactcaa ttatgcaccg gtctgaatga 60
 ataacatgtg gtttgctgcg cccatggggt cgccaccatg cgccctaggg ctcttttgct 120
 gttgttcctc ttgtttctgc ctatgttgcc cgcgccaccg accggtcagc cgtctggccg 180
 ccgtcgtggg cggcgcagcg gcggtaccgg cggtggtttc tggggtgacc gggttgattc 240
 tcagcccttc gcaatccctt atattcatcc aaccaacccc tttgccccag acgttgccgc 300

<210> 235
 <211> 297
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {840453p} shown in Figure 9B

<400> 235
 acagagacta ttaaacctgt acttgatctc acaaattcca tcatacagcg ggtggaatga 60
 ataacatgtc ttttgcatcg cccatgggat caccatgcgc cctagggctg ttctgttggt 120
 gttcctcatg tttctgccta tgctgcccgc gccaccggcc ggtcagccgt ctggccgctg 180
 ccgtgggcgg cgcagcggcg gtgcggcgcg tggtttctgg agtgacaggg ttgattctca 240
 gcccttcgcc ctcccctata ttcattcaac caaccccttc gccgccgatg tcgtttc 297

<210> 236
 <211> 300
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p Consensus shown in Figure 9B

<220>
 <221> variation
 <222> (1)..(300)
 <223> The nucleotide identity of each n is indicated in
 Figure 9B

<400> 236
 acngagncnn tnaancnnt nctnganntn acanantcna tnntnnnnncg gnnngaattga 60
 ataacatgtn ntttgcnnncg cccatgggnt nnnnaccatg cgccctnggn ctnttntgnt 120
 gntgntcctc ntgtttntgc ctatnttgcc cgcgccaccg nccggtcagc cgtctggccg 180
 ncgncgtggg cggcgagcgc gcggtncggg cggtggtttc tggngtgacn gggttgattc 240
 tcagcccttc gcntccctt atattcatcc aaccaacccc ttngcncng angtnnnnnnc 300

<210> 237
 <211> 250
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {hpea} shown in Figure 9C

<400> 237
 agcgcttacc ctgtttaacc ttgctgacac cctgcttggc ggtctaccga cagaattgat 60
 ttgctcggct ggtggccagc tgttctactc tcgccccgtc gtctcagcca atggcgagcc 120
 gactgttaag ctgtatacat ctgtggagaa tgctcagcag gataagggtta ttgcaatccc 180
 gcatgacatc gacctcgggg aatcccgtgt agttattcag gattatgaca accaacaatga 240
 gcaggaccga 250

<210> 238
 <211> 250
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {hpeuigh} shown in Figure 9C

<400> 238

agcgcttacc ctgtttaacc ttgctgacac cctgcttggc ggtctaccga cagaattgat 60
 ttcgctgggt ggtggccagc tgttctactc tcgccccgtc gtctcagcca atggcgagcc 120
 gactgttaag ctgtatacat ctgtagagaa tgctcagcag gataagggtg ttgcaatccc 180
 gcatgacatc gacctcgggg aatctcgagt tgttattcag gattatgaca accaacaatga 240
 gcaggaccgg 250

<210> 239
 <211> 250
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {hpesvp} shown in Figure 9C

<400> 239
 agccctcacc ctgttcaacc ttgctgacac tctgcttggc ggcttgccga cagaattgat 60
 ttcgctgggt ggtggccagc tgttctactc ccgtcccgtt gtctcagcca atggcgagcc 120
 gactgttaag ttgtatacat ctgtagagaa tgctcagcag gataagggtg ttgcaatccc 180
 gcatgacatt gacctcggag aatctcgtgt gggtattcag gattatgata accaacaatga 240
 acaagatcgg 250

<210> 240
 <211> 250
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> 3p.pile {hpenssp} shown in Figure 9C

<400> 240
 agctctaaca ttacttaacc ttgctgacac gctcctcggc gggctcccga cagaattaat 60
 ttcgctgggt ggcgggcaac tgttttattc ccgcccgtt gtctcagcca atggcgagcc 120
 aaccgtgaag ctctatacat cagtggagaa tgctcagcag gataagggtg ttgctatccc 180
 ccacgatatc gatcttggtg attcgcgtgt gggtattcag gattatgaca accagcatga 240
 gcaggatcgg 250

<210> 241
 <211> 250
 <212> DNA
 <213> Hepatitis E virus

<220>

<223> 3p.pile {840453p} shown in Figure 9C

<400> 241

```
tgccctgact ctgtttaatc ttgetgatac gcttcttggt ggtttaccga cagaattgat 60
ttcgtcggct ggggggtcaac tgttttactc ccgccctgtt cagaattgat ttcgtcggct 120
gggggtcaac tgttttactc ccgccctgtt tgcgcagcaa gacaaggga tcaccattcc 180
acacgacata gatttaggtg actcccgtgt gggtatccag gattatgata accagcacga 240
acaagatcga
```

250

<210> 242

<211> 250

<212> DNA

<213> Hepatitis E virus

<220>

<223> 3p Consensus shown in Figure 9C

<220>

<221> variation

<222> ()..(250)

<223> The nucleotide identity of each n is indicated in Figure 9C

<400> 242

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ngcncnacb ntnntnaanc ttgetganac nctnctnggn ggnntnccga cagaattnat 60
ttcgtcggct ggnggncanc tgttntantc ncgncngtn gtctcngcca atggcgagcc 120
nacngtnaag ntntanacat cngtngagaa tgcncagcan ganaagggnn tnnonatancc 180
ncanganatn ganntnggng antcncngt ngtnatncag gattatgana accancanga 240
ncangancgn
```

250

<210> 243

<211> 418

<212> DNA

<213> Hepatitis E virus

<220>

<223> Aulol-wlabolpl.pat

<220>

<221> CDS

<222> (3)..(416)

<400> 243

```
ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aat 47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    1             5             10             15
```


tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtg	95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val	
20 25 30	
cag act gag atc ctt att aac ttg atg caa cct cgg cag ctg gtg ttc	143
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cga cct gag gtg ctt tgg aat cat ccc att cag cgg gtt atc cat aat	191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gag tta gaa caa tac tgc cgg gcc cgg gcc ggc cgt tgc cta gag gtg	239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75	
ggg gcc cac cca agg tcc att aac gat aac ccc aat gtt ttg cac cgg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
80 85 90 95	
tgt ttt ctg cga ccg gtc ggg agg gat gtt cag cgc tgg tac tct gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggc cct gcg gct aac tgc cgc cgc tcc gct ttg cgt ggc	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctt ccc ccc gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	
<210> 244	
<211> 138	
<212> PRT	
<213> Hepatitis E virus	
<400> 244	
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser	
1 5 10 15	
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln	
20 25 30	
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg	
35 40 45	
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu	
50 55 60	
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly	
65 70 75 80	
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys	
85 90 95	

Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
 100 105 110

Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
 115 120 125

Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
 130 135

<210> 245
 <211> 197
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> Aulo2-wlao2.pat

<220>
 <221> CDS
 <222> (2) .. (196)

<400> 245
 g aca gaa ttr att tgc tgc gct ggg gga cag tta ttc tac tcc cgc cct 49
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15

gty gtc tca gcc aat ggc gag ccg act gtt aaa tta tat aca tct gta 97
 Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30

gag aat gcg cag cag gac aag ggg att gcc atc cca cat gat ata gat 145
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

ctg ggc gac tct cgt gtg gtg atc cag gat tat gay aac car cay gaa 193
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

caa g 197
 Gln
 65

<210> 246
 <211> 65
 <212> PRT
 <213> Hepatitis E virus

<400> 246
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15

Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp

35

40

45

Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

Gln
 65

<210> 247

<211> 418

<212> DNA

<213> Hepatitis E virus

<220>

<223> Arl01- f73olpl.pat

<220>

<221> CDS

<222> (3)..(416)

<400> 247

ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aac 47
 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
 1 5 10 15

tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtg 95
 Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
 20 25 30

cag acc gag att ctt att aac cta atg caa ccc cgg cag ctg gtt ttt 143
 Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
 35 40 45

cgt cct gag gtg ctt tgg aac cat cct atc cag cgg gtt att cat aat 191
 Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
 50 55 60

gag tta gaa cag tac tgt cgg gct cgg gct ggt cgc tgc cta gag gtc 239
 Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
 65 70 75

ggg gcc cac cca agg tcc att aat gat aac cct aat gtt ttg cac cgg 287
 Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
 80 85 90 95

tgc ttc cta cga cca gtc ggg agg gat gtt caa cgt tgg tat tcc gcc 335
 Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
 100 105 110

ccc acc cgc ggt cct gct gcc aac tgc cgc cgt tcc gct ctg cgc ggc 383
 Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
 115 120 125

ctc cct ccc gtc gac cgc act tac tgt yty gat gg 418
 Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
 130 135

<210> 248
 <211> 138
 <212> PRT
 <213> Hepatitis E virus

<400> 248
 Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
 1 5 10 15
 Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
 20 25 30
 Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
 35 40 45
 Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
 50 55 60
 Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
 65 70 75 80
 Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
 85 90 95
 Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
 100 105 110
 Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
 115 120 125
 Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
 130 135

<210> 249
 <211> 145
 <212> DNA
 <213> Hepatitis E virus

<220>
 <223> Arl-f73o2p2.pat

<220>
 <221> CDS
 <222> (1)..(144)

<400> 249
 gty gtc tcr gcc aat ggc gag ccg act gtt aag cta tat aca tct gta 48
 Xaa Val Xaa Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 1 5 10 15
 gag aac gcg cag cag gat aaa ggg atc gcc att cca cac gat ata gat 96
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 20 25 30

[illegible]

tgc ttc tta cga cca gtc ggg agg gat gtc caa cga tgg tac tca gcc 335
 Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
 100 105 110

ccc act cgc ggc cct gcg gct aat tgc cgt cgt tcc gct ttg cgt ggt 383
 Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
 115 120 125

ctc cct cct gtc gac cgc act tac tgt yty gat gg 418
 Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
 130 135

<210> 252

<211> 138

<212> PRT

<213> Hepatitis E virus

<400> 252

Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
 1 5 10 15

Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
 20 25 30

Thr Glu Ile Leu Ile Asn Leu Met Xaa Pro Arg Xaa Leu Val Phe Arg
 35 40 45

Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
 50 55 60

Leu Glu Gln Tyr Cys Arg Thr Arg Ala Gly Arg Cys Leu Glu Val Gly
 65 70 75 80

Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Xaa His Arg Cys
 85 90 95

Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
 100 105 110

Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
 115 120 125

Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
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<210> 253

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<212> DNA

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<221> CDS

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<400> 253

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1

5

10

15

gtc gtc tca gcc aat ggc gag ccg act gtt aag ttg tat aca tct gtg 97
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val

20

25

30

gag aat gcg cag cag gat aaa gga atc gcc atc cca cac gac ata gat 145
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp

35

40

45

ctg ggc gat tcc cgt gtg gtt att cag gat tat gay aac car cay gaa 193
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu

50

55

60

caa g 197
 Gln
 65

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<211> 65

<212> PRT

<213> Hepatitis E virus

<400> 254

Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15

Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30

Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45

Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60

Gln
 65

<210> 255

<211> 23

<212> DNA

<213> Hepatitis E virus

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<223> HEVConsORF 1N-a1

<400> 255

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<210> 256
 <211> 25
 <212> DNA
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<220>
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<400> 256
 cytgytcrtg ytggttrtca taatc

25

<210> 257
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 <212> DNA
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<220>
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<400> 257
 cygccytkgc gaatgctgtg g

21

<210> 258
 <211> 25
 <212> DNA
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<220>
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<400> 258
 gytcrtygtg rtttrtcataa tcctg

25